

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: May 27, 2003, 18:25:46 ; Search time 19 Seconds

(without alignments)
1189.031 Million cell updates/sec

Title: US-08-994-468-6

Perfect score: 1242
Sequence: 1 MVLAPAWSPPTLYLLLL...RCGEVPPVPSQDLLVLRH 235

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

PIR73:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1 | 1242 | 100.0 | 235 | 2 | 138440 |
| 2 | 864.5 | 69.6 | 245 | 2 | 543293 |
| 3 | 834 | 67.1 | 178 | 2 | 139076 |
| 4 | 768.5 | 61.9 | 231 | 2 | A49265 |
| 5 | 606.5 | 48.8 | 220 | 2 | 543291 |
| 6 | 606.5 | 48.8 | 220 | 2 | 158343 |
| 7 | 93 | 7.5 | 1217 | 2 | T22672 |
| 8 | 92 | 7.4 | 661 | 1 | TNBE12 |
| 9 | 89.5 | 7.2 | 474 | 2 | T19543 |
| 10 | 89 | 7.2 | 387 | 2 | 148201 |
| 11 | 89 | 7.2 | 793 | 2 | 148201 |
| 12 | 88.5 | 7.1 | 238 | 2 | AB1990 |
| 13 | 88.5 | 7.1 | 1386 | 2 | T00257 |
| 14 | 88 | 7.1 | 753 | 2 | T00532 |
| 15 | 87.5 | 7.0 | 479 | 1 | A32250 |
| 16 | 87 | 7.0 | 910 | 2 | A53137 |
| 17 | 86.5 | 6.9 | 590 | 2 | A40437 |
| 18 | 86 | 6.9 | 299 | 2 | T17832 |
| 19 | 86 | 6.9 | 485 | 2 | A33647 |
| 20 | 86 | 6.9 | 746 | 2 | T28004 |
| 21 | 85 | 6.8 | 289 | 2 | A87646 |
| 22 | 85 | 6.8 | 366 | 2 | A37374 |
| 23 | 84 | 6.8 | 263 | 2 | T03162 |
| 24 | 84 | 6.8 | 757 | 2 | A39283 |
| 25 | 83.5 | 6.7 | 189 | 2 | E75630 |
| 26 | 83.5 | 6.7 | 530 | 2 | A45650 |
| 27 | 83 | 6.7 | 1509 | 2 | T19486 |
| 28 | 82.5 | 6.6 | 418 | 2 | T19800 |
| 29 | 82.5 | 6.6 | 426 | 2 | 136948 |

ALIGNMENTS

| | | | | | | |
|----|------|-----|------|---|--------|--------------------|
| 30 | 82.5 | 6.6 | 512 | 2 | D40829 | activin receptor 1 |
| 31 | 82.5 | 6.6 | 513 | 2 | J01484 | activin receptor p |
| 32 | 82 | 6.6 | 106 | 2 | T06479 | proline/leucine-ri |
| 33 | 82 | 6.6 | 854 | 2 | T23837 | hypothetical prote |
| 34 | 81.5 | 6.6 | 485 | 2 | C73460 | hypothetical prote |
| 35 | 81.5 | 6.6 | 488 | 2 | S13423 | stromelysin 3 (EC |
| 36 | 81.5 | 6.6 | 958 | 2 | T13593 | hypothetical prote |
| 37 | 81.5 | 6.6 | 1119 | 2 | T50995 | related to cytocte |
| 38 | 81 | 6.5 | 196 | 2 | B48232 | cysteine-rich exte |
| 39 | 81 | 6.5 | 209 | 2 | A48332 | hypothetical prote |
| 40 | 81 | 6.5 | 294 | 2 | A12016 | probable transpos |
| 41 | 81 | 6.5 | 388 | 2 | S15591 | class I cytokinase |
| 42 | 80.5 | 6.5 | 428 | 1 | EHU | hypothetical prote |
| 43 | 80.5 | 6.5 | 636 | 2 | JM0047 | hypothetical prote |
| 44 | 80.5 | 6.5 | 1176 | 2 | T49482 | |
| 45 | 80.5 | 6.5 | 1306 | 2 | T13592 | |

RESULT 1
138440
flt3 ligand - human
C:Species: Homo sapiens (man)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 01-Dec-2000
C:Accession: I38440; 139075; 543292
R:Lyman, S.D.; James, L.; Johnson, L.; Brasel, K.; de Vries, P.; Escobar, S.S.; Downe
Blood 83, 2795-2801, 1994
A:Title: Cloning of the human homologue of the murine flt3 ligand: a growth factor fo
A:Reference number: I38440; MUID:94235842; PMID:8180375
A:Accession: I38440
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-235 <RES>
A:Cross-references: EMBL:U03658; NID:9494978; PIDN:AAA19825.1; PID:9494979
R:Lyman, S.D.; Stocking, K.; Davison, B.; Fletcher, F.; Johnson, L.; Escobar, S.
Oncogene 11, 1165-1172, 1995
A:Title: Structural analysis of human and murine flt3 ligand genomic loci.
A:Reference number: 139075; MUID:96032581; PMID:7566577
A:Accession: 139075
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-235 <RES>
A:Cross-references: EMBL:U29874; NID:91072036; PIDN:AAA90949.1; PID:91072037
R:Hannum, C.; Culpepper, J.; Campbell, D.; McClanahan, T.; Zurawski, S.; Baran, J.F.;
felt, A.; Muench, M.; Kellner, G.; Nemikawa, R.; Rennick, D.; Roncarolo, M.G.; Zlotnik
Nature 368, 643-648, 1994
A:Title: Ligand for FLT3/FLK2 receptor tyrosine kinase regulates growth of haematopo
A:Reference number: 543290; MUID:94195428; PMID:8145851
A:Accession: 543292
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-71, 'A', '73-235 <HAN>
A:Cross-references: GB:U04806; NID:9483844; PIDN:AAA17999.1; PID:9483845
A:Note: The authors translated the codon AGT for residue 25 as Met
C:Genetics:
A:Introns: 11/3; 48/3; 66/3; 114/3; 161/1; 220/3
Query Match 100.0%; Score 1242; DB 2; Length 235;
Best Local Similarity 100.0%; Pred. No. 5, 4e-99;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 MVLAPAWSPPTLYLLLLSSGSGTDCSROHSPISDFAVKIRELSDYLLQDYPYV 60
1 MVLAPAWSPPTLYLLLLSSGSGTDCSROHSPISDFAVKIRELSDYLLQDYPYV 60
DB 1 MVLAPAWSPPTLYLLLLSSGSGTDCSROHSPISDFAVKIRELSDYLLQDYPYV 60
61 ASNLODEELCGIMRLVLAQRMERLKTAVAGSKMGLERVTETHTFKCAFQPPSPCL 120
61 ASNLODEELCGIMRLVLAQRMERLKTAVAGSKMGLERVTETHTFKCAFQPPSPCL 120
DB 61 ASNLODEELCGIMRLVLAQRMERLKTAVAGSKMGLERVTETHTFKCAFQPPSPCL 120
121 REVQINISRLQETSEQVALKPMWITRONFSRCLQLQCPQSSSTLPWSPRPLEATAPY 180
121 REVQINISRLQETSEQVALKPMWITRONFSRCLQLQCPQSSSTLPWSPRPLEATAPY 180

Db 121 RFVQNTISRLQETSEQLVAKPWITRONFSRCLELOCOPDSSSTLPWPMSRPRLPEAT 180

QY 181 APOPLLILLLLPVGLLLAAACLMQRTRRRTPRGEQVPVPSPDOLLVH 235

Db 181 APOPLLILLLLPVGLLLAAACLMQRTRRRTPRGEQVPVPSPDOLLVH 235

RESULT 2

S43293

FLI3/FLK2 ligand (clone S109) - human

C:Species: Homo sapiens (man)

C>Date: 20-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 17-Mar-1999

C:Accession: S43293

R:Hanum, C.; Culpepper, J.; Campbell, D.; McClanahan, T.; Zurawski, S.; Bazan, J.F.; Kelf, A.; Muench, M.; Kellner, G.; Nankkawa, R.; Rennick, D.; Roncarolo, M.G.; Zlotnik, A. Nature 368, 643-648, 1994

A:Title: Ligand for FLI3/FLK2 receptor tyrosine kinase regulates growth of hematopoietic

A:Reference number: S43290; MUID:94195428; PMID:8145851

A:Accession: S43293

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-245 <HAN>

A>Note: the authors translated the codon AGR for residue 25 as Met

Query Match 69.6%; Score 864.5; DB 2; Length 245;

Best Local Similarity 73.0%; Pred. No. 1.2e-66;

Matches 176; Conservative 7; Mismatches 27; Indels 31; Gaps 3;

QY 1 MYLAPAMSPFTYLLILLLSSGLSGTDCSFQHSPISSDFAVKIRELSYLLQDYPTV 60

Db 1 MYLAPAMSPFTYLLILLLSSGLSGTDCSFQHSPISSDFAVKIRELSYLLQDYPTV 60

QY 61 ASNLODEELCGGLMRVLAORMERLKTVAAGSKMOGLLEVNTEIHFTVTKCAFQPPSCL 120

Db 61 ASNLODEELCGGLMRVLAORMERLKTVAAGSKMOGLLEVNTEIHFTVTKCAFQPPSCL 120

QY 121 RFVQNTISRLQETSEQLVAKPWITRONFSRCLELOCOPDSSSTLPWPMSRPRLPEAT 180

Db 121 RFVQNTISRLQETSEQLVAKPWITRONFSRCLELOCOPDSSSTLPWPMSRPRLPEAT 177

QY 181 APOPLLILLLLPVGLLLAAACLMQRTRRRTPRGEQVPVPSP 227

Db 178 WPRHPEDTAEHARGESP-----ARQCIANTQKRLANGRLNAPLIPSP 222

QY 228 Q 228

Db 223 E 223

RESULT 3

FLI3 ligand alternatively spliced isoform - human

C:Species: Homo sapiens (man)

C>Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000

C:Accession: I39076

R:Lyman, S.D.; Stocking, K.; Davison, B.; Fletcher, F.; Johnson, L.; Escobar, S. Oncogene 11, 1165-1172, 1995

A:Title: Structural analysis of human and murine flt3 ligand genomic loci.

A:Reference number: I39075; MUID:96032581; PMID:7565977

A:Accession: I39076

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-178 <RES>

A:Cross-References: EMBL:U29874; NID:g1072036; PIDN:AAA90950.1; PID:g1072038

C:Genetics:

A:introns: 11/3; 48/3; 66/3; 114/3; 161/1

Query Match 67.1%; Score 834; DB 2; Length 178;

Best Local Similarity 100.0%; Pred. No. 3.3e-64;

Matches 160; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYLAPAMSPFTYLLILLLSSGLSGTDCSFQHSPISSDFAVKIRELSYLLQDYPTV 60

Db 1 MYLAPAMSPFTYLLILLLSSGLSGTDCSFQHSPISSDFAVKIRELSYLLQDYPTV 60

Db 1 MYLAPAMSPFTYLLILLLSSGLSGTDCSFQHSPISSDFAVKIRELSYLLQDYPTV 60

QY 61 ASNLODEELCGGLMRVLAORMERLKTVAAGSKMOGLLEVNTEIHFTVTKCAFQPPSCL 120

Db 61 ASNLODEELCGGLMRVLAORMERLKTVAAGSKMOGLLEVNTEIHFTVTKCAFQPPSCL 120

QY 121 RFVQNTISRLQETSEQLVAKPWITRONFSRCLELOCOP 160

Db 121 RFVQNTISRLQETSEQLVAKPWITRONFSRCLELOCOP 160

RESULT 4

A49265

FLI3/FLK-2 ligand precursor - mouse

C:Species: Mus musculus (house mouse)

C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 08-Oct-1999

C:Accession: A49265; I49347; I49346; S43290

R:Lyman, S.D.; James, L.; Vanden Bos, T.; de Vries, P.; Brasel, K.; Gliniak, B.; Holl Cell 75, 1157-1167, 1993

A:Title: Molecular cloning of a ligand for the flt3/flk-2 tyrosine kinase receptor: a

A:Reference number: A49265; MUID:94084791; PMID:7505204

A:Accession: A49265

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-231 <LYM>

A:Cross-References: GB:L23636; NID:g439441; PIDN:AAA9436.1; PID:g439442

R:Lyman, S.D.; Stocking, K.; Davison, B.; Fletcher, F.; Johnson, L.; Escobar, S. Oncogene 11, 1165-1172, 1995

A:Title: Structural analysis of human and murine flt3 ligand genomic loci.

A:Reference number: I39075; MUID:96032581; PMID:7565977

A:Accession: I49347

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-163; 'G', 165, 'HYAG' <RES>

A:Cross-References: EMBL:U29875; NID:g1072039; PIDN:AAA90952.1; PID:g1072041

A:Accession: I49346

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-197; 'L', 198-231 <RES>

A:Cross-References: EMBL:U29875; NID:g1072039; PIDN:AAA90951.1; PID:g1072040

R:Hanum, C.; Culpepper, J.; Campbell, D.; McClanahan, T.; Zurawski, S.; Bazan, J.F.; Kelf, A.; Muench, M.; Kellner, G.; Nankkawa, R.; Rennick, D.; Roncarolo, M.G.; Zlotnik Nature 368, 643-648, 1994

A:Title: Ligand for FLI3/FLK2 receptor tyrosine kinase regulates growth of hematopoietic

A:Reference number: S43290; MUID:94195428; PMID:8145851

A:Accession: S43290

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-197; 'L', 198-231 <HAN>

A:Experimental source: clone T110

A>Note: the sequence from Flg. 2c is inconsistent with that from Flg. 2a in having 4-

C:Genetics:

A:introns: 11/3; 49/3; 67/3; 115/3; 164/1; 224/3

C:Keywords: transmembrane protein

Query Match

61.9%; Score 768.5; DB 2; Length 231;

Best Local Similarity 70.3%; Pred. No. 1.8e-58;

Matches 163; Conservative 17; Mismatches 43; Indels 9; Gaps 4;

QY 1 MYLAPAMSPFTYLLILLLSSGLSGTDCSFQHSPISSDFAVKIRELSYLLQDYPTV 59

Db 1 MYLAPAMSPFTYLLILLLSSGLSGTDCSFQHSPISSDFAVKIRELSYLLQDYPTV 60

QY 60 VASNLODEELCGGLMRVLAORMERLKTVAAGSKMOGLLEVNTEIHFTVTKCAFQPPSCL 119

Db 61 VASNLODEELCGGLMRVLAORMERLKTVAAGSKMOGLLEVNTEIHFTVTKCAFQPPSCL 120

QY 120 LRFVQNTISRLQETSEQLVAKPWITR--QNFSCLELOCOPDSSSTLPWPMSRPRLPEAT 177

Db 120 LRFVQNTISRLQETSEQLVAKPWITR--QNFSCLELOCOPDSSSTLPWPMSRPRLPEAT 177

QY 121 LRFVQNTISRLQETSEQLVAKPWITR--QNFSCLELOCOPDSSSTLPWPMSRPRLPEAT 180

Db 121 LRFVQNTISRLQETSEQLVAKPWITR--QNFSCLELOCOPDSSSTLPWPMSRPRLPEAT 180

QY 178 APTAPPP--LLLLLPVGLLLAAACLMQRTRRRTPRGEQVPVPSP 227

OY 124 QTNISRLQETSEOLVAKPWITRONFSRCLELOCQDDSTLPPMSP-RPLEATAPAP 182
 Db 198 NSDYGICQELREALGAVQKYM---YFMR-----PDDPTNPSDFRIRFQETIAAYAT 247
 OY 183 QPRLILLLLPVGILLAAWCLMORTRRTPRGSEVPVPSODLL 231
 Db 248 GYGMMLFLVDVDD---ARVCRLKLQFRIRNGPRASV---IPDDL 287

RESULT 9

T19543
 hypothetical protein C28D4.2 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans
 C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C/Accession: T19543
 R/McMurray, A.
 submitted to the EMBL Data Library, November 1996

A/Accession: T19543
 A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA
 A/Residues: 1-474 <NLS>

A/Cross-references: EMBL:282259; PIDN:CAB05129.1; GSPDB:GN00022; CESP:C28D4.2
 C/Experimental source: clone C28D4

A/Genes: CESP:C28D4.2

A/Map position: 4
 A/Intons: 26/3; 72/3; 118/2; 169/1; 203/2; 240/2; 262/3; 298/3; 342/2; 391/3

Query Match 7.2%; Score 89.5; DB 2; Length 474;

Best Local Similarity 24.1%; Pred. No. 5.5;
 Matches 59; Conservative 29; Mismatches 82; Indels 75; Gaps 15;

OY 27 TQDC-----SFQHS-PISSDFAVKIREL-SDYLLQDYPTVANSIODELGGIWLRL 76
 Db 65 TTDCVDLKKVFSKFDSSAPISGEILFRARFLCAKYL-----GGAWRK 106
 OY 77 VLAQRMMERLKTAVGSMQGLLENVETHFVVKCAFOPPBSCLR-FVQTNISRLQET- 134
 Db 107 VKIEEF--RIRATIGG-MSNLLFLVELPAH-LPIQMEPEKALRVHCQSDIDQLSESV 162
 OY 135 -----SEQLVAKPWITRONFSRCLELOC-----QDDSTLPPMSPR-PLDATA 178
 Db 163 VFTLLSRNIGPKKGLVFPFGREGQFIPSALOCLEISKGLSLIPIYARVHTLDAPL 222
 OY 179 PTAPOPRLILLLLPVGLLLAAWCLMORTRRTPR-RPGE-----QVPVPSPOD 229
 Db 223 PKEBQ-----TLGTARQWIERF-----KKWPAEGEPIMVTLQAKVPSDYFST 266
 OY 230 LLAVE 234
 Db 267 ITVAQ 271

RESULT 10

I48201
 adhalin - golden hamster

C/Species: Mesocricetus auratus (golden hamster)
 C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 20-Jun-2000
 C/Accession: I48201
 R/Roberds, S.L.; Campbell, K.P.
 FEBS Lett. 364; 245-249, 1995

A/Title: Adhalin mRNA and cDNA sequence are normal in the cardiomyopathic hamster.
 A/Reference number: I48201; MUID:95278335; PMID:7758576

A/Accession: I48201
 A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA
 A/Residues: 1-387 <RES>

A/Cross-references: EMBL:Q21677; NID:9726481; PIDN:AAA81645.1; PID:9726482
 C/Superfamily: mouse adhalin

Query Match 7.2%; Score 89; DB 2; Length 387;
 Best Local Similarity 23.4%; Pred. No. 4.8;

Matches 71; Conservative 26; Mismatches 97; Indels 110; Gaps 14;

OY 11 TTYILLILLSSGTCDDCSFQHSPISSDFAVKIRELSDYLLQDYPTVANSIODEELC 70
 Db 115 TTRORLLILLI-----BDPEGRLPYQAEFLVRSHDVEEVL---PSTPANRL-TAL 161
 OY 71 GGLWRL-----VLAQRMMERLKTAVGSMQGLLENVETHFV- 110
 Db 162 GGLWELGELQDLNITSALDRGRVPLPIEGREGVYIKVGSATPTSTCLKVAVSPDSTAR 221
 OY 111 CAFOPPP--SC-----LRFVQTNISRLQETSEOLVAKPWITRONFSRCLELOCOPD 161
 Db 222 CAQCGPPLLSQCYDSLAPHFVDMCVSLVSKSVPEPLD-----EVPTGCD 266
 OY 162 SSTLPPMSPRPLEAT-----APTAPOPRLILLLLPVGILLAAWCL- 204
 Db 267 GILHDFPCPTPEATGDFLADALVTLVPLVALLL---TLILAAYIMCCREGOLKRD 323
 OY 205 -----LHWQTRRRTRPR-----GEQVPP-VPSPO-DLL 231
 Db 324 MATSDIQVHHTHGNTEELROMAAREVVRPLSTLPMFNVRIGERLPPRVDASQVPLI 383
 OY 232 LVEN 235
 Db 384 LDQH 387

RESULT 11

S60735
 splicing factor SF3a 120K chain - human

C/Species: Homo sapiens (man)
 C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
 C/Accession: S60735; S60733
 R/Kraemer, A.; Mulhauser, F.; Wersig, C.; Groening, K.; Blube, G.

A/Title: Mammalian splicing factor SF3a120 represents a new member of the SURP family

A/Reference number: S60733; MUID:96079558; PMID:7489498

A/Accession: S60735
 A/Status: nucleic acid sequence not shown

A/Molecule type: mRNA

A/Residues: 1-793 <KRA>

A/Cross-references: EMBL:X85237; NID:9899297; PIDN:CAA59494.1; PID:9899298

A/Accession: S60733
 A/Molecule type: protein

A/Residues: 51-62; 82-94; 270-275; 397-414; 448-463 <KRA2>

A/Genes: GDB:SF3A120; PRP21; SAP114
 A/Cross-references: GDB:9955873

A/Map position: 22q12.1-22qter
 C/Superfamily: human splicing factor SF3a 120K chain; ubiquitin homology

C/Keywords: pre-mRNA splicing
 F;714-790/Domain: ubiquitin homology <UBH>

Query Match

Best Local Similarity 7.2%; Score 89; DB 1; Length 793;

Matches 67; Conservative 34; Mismatches 79; Indels 120; Gaps 17;

OY 4 LAPMSPTTYILLILLSSGTCDDCSFQHSPISSDFAVKIRELSDYLLQDYPTVANSI 63
 Db 401 LPPAPAPDEVIV-----SPITGE---KI-----PSAK 424
 OY 64 LODEELCGGLRLVLAQRMMERLKTAV- 107
 Db 425 MOEHRIG-----LLDRPRLWEQRODRSIREKQSDDEVYAPGLDISSILKQLMER-RTDFG 478
 OY 108 VTKA-----FQPPSCLRF-----VQTNISRLQETSEOLVAKPWIT 145
 Db 479 VEETAIKKIGEEIQRPEEKVTWDGSGSMARTQAAQANIT--LOEITAIHKAKGLV 536
 OY 146 -----TRONF--SRCLELOCOP-----DSTLPP-----PPMSPRPLEAT-----APT 180
 Db 537 PEDDTKEIKPSKNEIIPQDPPPSATINIPSSAPPIITSVPRPTMPBPVATTYVAVPV 596

OY 181 APQPLLLLLPVGLLLAAACLMWORT-----RTTPRGQVPP---VPSP 227
 Db 597 MRPMAVSVLRPPGVSIVAMPPIIHAPRINVPMPSPAPRIMAPRPPMIVTAPVAP 656

RESULT 12

AB1990

hypotheical protein all1471 (imported) - Nostoc sp. (strain PCC 7120)

C:Species: Nostoc sp.
 A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
 C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
 C:Accession: AB1990
 R:Kaneko, T.; Nakamura, Y.; Molk, C.P.; Kuritz, T.; Sasamoto, S.; Matsumoto, A.; Iriiguchi, N.; Shimizu, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
 DNA Res. 8, 205-213, 2001
 A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena
 A:Reference number: AB1807; MUID:21595285; PMID:11759840
 A:Accession: AB1990
 A:Status: Preliminary
 A:Molecule type: DNA
 A:Residues: 1738 <KUR>
 A:Cross-references: GB:BA000019; PIDN:BA877837.1; PID:g17135292; GSPDB:GN00179
 A:Experimental source: strain PCC 7120
 C:Genetics:
 A:Gene: all1471

Query Match 7.1%; Score 88.5; DB 2; Length 238;
 Best Local Similarity 20.8%; Pred. No. 3;
 Matches 44; Conservative 32; Mismatches 59; Indels 77; Gaps 9;

OY 34 HSPISDFAVIRELSDYLDY---PYVANSNLODELGLMLRYLQRMWERTKTA 90
 Db 84 HSKTTTYESINEYCNQYLKSYKKPLVIT-----QLG--W-----SQRIMRYKTYD 131
 OY 91 GSKMOGLIERVTEIHFYTKCAFOPPPSCLEFVQTNISRLD-----ETSEQ 137
 Db 132 DDDTDIDISPGISTEV-----VVRKIPRIVETPKIVKQKTEDITLES 174
 OY 138 LVALKPWITRQNFSCLELOCOPDSSTLPPW---SPRLENTAPAPOPPLLLLLLPV 194
 Db 175 POSLKP--TKPIPPKLEIPKSEDSKNIQRPRIIPSPKIKNSOPEAPRPV----- 223
 OY 195 GLLLAAACLMWORTRRTRPRGQVPPVPS 226
 Db 224 -----EPPKPMERVPKKPS 237

RESULT 13

T00257

hypotheical protein KIAA0476 - human

C:Species: Homo sapiens (man)
 C:Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 24-Jul-2000
 C:Accession: T00257
 R:Seiki, N.; Ohira, M.; Nagase, T.; Ishikawa, K.; Miyajima, N.; Nakajima, D.; Nomura, N.; DNA Res. 4, 345-349, 1997
 A:Title: Characterization of cDNA clones in size-fractionated cDNA libraries from human
 A:Reference number: Z14085; MUID:98116662; PMID:9455484
 A:Accession: T00257
 A:Status: Preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1386 <SEK>
 A:Cross-references: EMBL:AB007945; NID:g3413913; PIDN:BA432321.1; PID:g3413914
 A:Experimental source: Brain
 C:Genetics:
 A:Note: KIAA0476

Query Match 7.1%; Score 88.5; DB 2; Length 1386;
 Best Local Similarity 23.1%; Pred. No. 23;
 Matches 53; Conservative 28; Mismatches 85; Indels 63; Gaps 12;

OY 21 SSGLSGTCDFQSHSPISDFAVIRELSDYLDYPTVANSNLODELGLMLRL 76
 Db 1104 SAGASGSKDAVPPGPP-----GVLSDRRLCLA--LDEPOLCNGHMGASRR 1148

OY 77 VLAQRMERKTVAGSKMOGLIERVTEIHFYTKCAFOPPPSCLEFVQTNISRLDQTS 136
 Db 1149 VESGAMAYLSPVLKRLKLESLVENEGSEV-----LALPELPSAPRIFFMLINTFQRL-- 1201
 OY 137 QLVALKPWITRQNFSCLELOCOPDSSTLPPW---SPRLENTAPAPOPPLLLLLLPV 185
 Db 1202 RLPSILPLGLVLA-----CGPSHSQAPSPWLTFFDPASVQVRLMDVLTDPDNCSP 1253
 OY 186 LLLLLPVGLLLAAACLMWORTRRTRPRGQVPPVPSQDILLVE 234
 Db 1254 LTVL-----WRVHSQ--IFQRVVPG---VPVASLALLE 1284

RESULT 14

J00532

OP protein - Kennedy yellow mosaic virus

C:Species: Kennedy yellow mosaic virus
 C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 28-May-1999
 C:Accession: J00532
 R:Ding, S.; Keese, P.; Gibbs, A.
 J. Gen. Virol. 71, 925-931, 1990
 A:Title: The nucleotide sequence of the genomic RNA of Kennedy yellow mosaic tymovir
 A:Reference number: J00532; MUID:90218040; PMID:2324710
 A:Accession: J00532
 A:Molecule type: mRNA
 A:Residues: 1-753 <DIN>
 A:Cross-references: GB:D00637; NID:g221969; PIDN:BA400531.1; PID:q1000986; PID:g22197
 A:Experimental source: strain Jervis Bay isolate

Query Match 7.1%; Score 88; DB 2; Length 753;
 Best Local Similarity 22.3%; Pred. No. 12;
 Matches 41; Conservative 19; Mismatches 58; Indels 66; Gaps 7;

OY 100 RVNTEIHFYTKCAFOPPPSCLEFVQTNIS-----RLQETSEGLVALKWITR 147
 Db 420 RUSTOPPSSPQYSSPPSPRTDASGIQTPPLSPSKREKSLPPSHQ---PPSHSK 475
 OY 148 QNFSR-----CLELOCOPDSSTLPPWSPRLENTAPAPOPPLLLLLLPV----- 193
 Db 476 RNLRRSALPLPLPIHPTKTQPHRAVPPQ--TAGTPHPPPKTKPLNPKSQENRPS 533
 OY 194 -----VGLLLAAACLMWORTRRTRPRGQVPPVPS 226
 Db 534 PDVFDCCPSSPSSHVGVRRLLGSGISLPFLAW-----RRSPNAPNHLRPPPP 586
 OY 227 PQDL 230
 Db 587 PKRL 590

RESULT 15

A32290

Protein-tyrosine-phosphatase (EC 3.1.3.48) cdc25 homolog string - fruit fly (Drosophila)

C:Species: Drosophila melanogaster
 C:Date: 05-Oct-1989 #sequence_revision 25-Apr-1997 #text_change 11-Jun-1999
 C:Accession: A32290; S12008
 R:Edgar, B.A.; O'Farrell, P.H.
 Cell 57, 177-187, 1989
 A:Title: Genetic control of cell division patterns in the Drosophila embryo.
 A:Reference number: A32290; MUID:89195217; PMID:2702688
 A:Accession: A32290
 A:Molecule type: mRNA
 A:Residues: 1-479 <EDG>
 A:Cross-references: GB:M24909; NID:g158507; PIDN:AAA28916.1; PID:g158508
 R:Jimenez, J.; Almey, L.; Nurse, P.; Glover, D.M.
 EMBO J. 9, 3565-3571, 1990
 A:Title: Complementation of fission yeast cdc2(ts) and cdc25(ts) mutants identifies t
 A:Reference number: S12008; MUID:91006056; PMID:2120044
 A:Accession: S12008
 A:Molecule type: mRNA
 A:Residues: 1-227; A', 229-479 <JIM>
 A:Cross-references: EMBL:X57495; NID:g7706; PIDN:CAA40732.1; PID:g7707

C:Genetics:

A:Gene: FlyBase:stg

A:Cross-references: FlyBase:FBgn0003525

C:Function:

A:Description: catalyzes hydrolysis of peptidyl-phosphotyrosine to peptidyl-tyrosine and

A:Note: cdc25 activates the cdc2 protein kinase by dephosphorylating it

C:Superfamily: protein-tyrosine-phosphatase string; cdc25-type protein-tyrosine-phosphat

C:Keywords: cell cycle control; mitosis; phosphoprotein; phosphoric monoester hydrolase;

F:252-456/Domain: cdc25-type protein-tyrosine-phosphatase homology <ppp>

F:379/Active site: Cys (phosphocysteine intermediate) #status predicted

F:385/Binding site: substrate phosphate (Arg) #status predicted

Query Match

Best Local Similarity 7.0%; Score 87.5; DB 1; Length 479;

Matches 56; Conservative 34; Mismatches 76; Indels 79; Gaps 14;

QY 1 MTYLPAMSPFTYILL--LLLSGSLGTQDCSFOHSPISSDPAVKIRELSDTYLLQDP 57
 DB 72 MGLSPGSGPQRFOYVQPKILPAMGVSS-----DHTPARS-FRI-FNSILSS-----T 117
 QY 58 VTVASNLQDELEGGLWRLVLAQRMERLKTVAGSKMOGLLERVNTREIHFVTKCAFQPP 117
 DB 118 CSMESSWDE-----YMELFEMESQSQ-----GTALGF-----P 146
 QY 118 SCURFVQTNISRLQETSEQLVAKP---WITQNSRCLQL-OCOPDSSTLPPEWSPRP 173
 DB 147 SGLN-----SLISGQIKEQPAKSPAGLSMRPVSVRCLSMTESNTNSTTTPPKTPE- 199
 QY 174 LEATAPTA---POPPLLLLLLPVGLLLAAACLMQRTRRRTPRRGEOVPPVPSQDL 230
 DB 200 ---TANCCFRPPEP-----ASANCSPISQSKRHRCATVEKENCPAPSPLSQ 242
 QY 231 LLYEH 235
 DB 243 VTISH 247

Search completed: May 27, 2003, 18:27:59
 Job time : 22 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: May 27, 2003, 18:25:26 ; Search time 11 Seconds
(without alignments)
886.085 Million cell updates/sec

Title: US-08-994-468-6
Perfect score: 1242
Sequence: 1 MTYLAPAMSPFTYLLILL...RPGQVPPVSPDOLLVEH 235

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|---------------|--------------------|
| 1 | 1242 | 100.0 | 235 | 1 FLJL_HUMAN | P49771 homo sapien |
| 2 | 768 | 61.8 | 232 | 1 FLJL_MOUSE | P49772 mus musculu |
| 3 | 92 | 7.4 | 661 | 1 AT12_VZVD | P09264 varicella-z |
| 4 | 89.5 | 7.2 | 941 | 1 GBR2_HUMAN | O75899 homo sapien |
| 5 | 89 | 7.2 | 387 | 1 SGCA_MESAU | O64255 mesocricetu |
| 6 | 89 | 7.2 | 793 | 1 S3AL_HUMAN | O15459 homo sapien |
| 7 | 87.5 | 7.0 | 415 | 1 TNR3_MOUSE | P50284 mus musculu |
| 8 | 87.5 | 7.0 | 479 | 1 WPIP_DROME | P20483 drosophila |
| 9 | 87 | 7.0 | 910 | 1 DDRI_RAT | O63474 rattus norv |
| 10 | 87 | 7.0 | 911 | 1 DDRI_MOUSE | O28181 bos taurus |
| 11 | 86.5 | 6.9 | 1394 | 1 CNG4_BOVIN | P21997 volvox cart |
| 12 | 86 | 6.9 | 485 | 1 SSGP_VOLCA | O972d1 homo sapien |
| 13 | 85 | 6.8 | 282 | 1 ATFS_HUMAN | P13599 rattus norv |
| 14 | 85 | 6.8 | 366 | 1 FCCN_RAT | O61329 mus musculu |
| 15 | 84.5 | 6.8 | 3726 | 1 ABFL_MOUSE | O99583 homo sapien |
| 16 | 84 | 6.8 | 582 | 1 MNT_HUMAN | O99583 homo sapien |
| 17 | 84 | 6.8 | 732 | 1 YF48_HUMAN | O99583 homo sapien |
| 18 | 84 | 6.8 | 1234 | 1 NPHN_RAT | O99583 homo sapien |
| 19 | 83.5 | 6.7 | 671 | 1 Z282_HUMAN | O99583 homo sapien |
| 20 | 83 | 6.7 | 758 | 1 VEGC_HUMAN | O99583 homo sapien |
| 21 | 82 | 6.6 | 2167 | 1 SHK1_RAT | O99583 homo sapien |
| 22 | 81.5 | 6.6 | 488 | 1 MNT_HUMAN | O99583 homo sapien |
| 23 | 81.5 | 6.6 | 591 | 1 MNT_MOUSE | O99583 homo sapien |
| 24 | 81.5 | 6.6 | 2124 | 1 Y192_HUMAN | O99583 homo sapien |
| 25 | 81 | 6.5 | 283 | 1 ATFS_MOUSE | O70191 mus musculu |
| 26 | 81 | 6.5 | 387 | 1 SGCA_MOUSE | P82350 mus musculu |
| 27 | 81 | 6.5 | 428 | 1 EPC_HUMAN | P01854 homo sapien |
| 28 | 81 | 6.5 | 1248 | 1 DIAL_HUMAN | O60610 homo sapien |
| 29 | 80.5 | 6.5 | 1402 | 1 IFAG_RABIT | P41110 oryctolagus |
| 30 | 80 | 6.4 | 397 | 1 CERD_STRCL | P18849 streptomyce |
| 31 | 80 | 6.4 | 940 | 1 GBR2_RAT | O88871 rattus norv |
| 32 | 80 | 6.4 | 1174 | 1 KPC1_COCHIE | O42632 cochlidozou |
| 33 | 80 | 6.4 | 1794 | 1 YAVL_SCHPO | Q10172 schizosacch |

| | | | | | |
|----|------|-----|------|--------------|---------------------|
| 34 | 79 | 6.4 | 805 | 1 YGN6_YEAST | P53086 saccharomyce |
| 35 | 78.5 | 6.3 | 251 | 1 HXB4_HUMAN | P17483 homo sapien |
| 36 | 78.5 | 6.3 | 382 | 1 AYRB_RAT | P38445 rattus norv |
| 37 | 78.5 | 6.3 | 387 | 1 SGCA_RABIT | O28686 oryctolagus |
| 38 | 78.5 | 6.3 | 913 | 1 DDRI_HUMAN | O08345 h epithelia |
| 39 | 78.5 | 6.3 | 1180 | 1 ATYL_HUMAN | O98211 homo sapien |
| 40 | 78 | 6.3 | 205 | 1 CYSR_SYNY3 | O55854 synchocyst |
| 41 | 78 | 6.3 | 566 | 1 TS13_MOUSE | O01755 mus musculu |
| 42 | 77.5 | 6.2 | 341 | 1 PLSX_VIBCH | O9kq44 vibrio chol |
| 43 | 77.5 | 6.2 | 1885 | 1 FAS2_CANAL | P43098 c fatty aci |
| 44 | 77.5 | 6.2 | 2004 | 1 MZ2_HUMAN | O92794 homo sapien |
| 45 | 77 | 6.2 | 195 | 1 CORA_HPBVE | P29178 hepatitis b |

ALIGNMENTS

RESULT 1
FLJL_HUMAN
ID FLJL_HUMAN STANDARD: PRT; 235 AA.
AC P49771:
DT 01-OCT-1996 (rel. 34, Created)
DT 01-OCT-1996 (rel. 34, Last sequence update)
DT 15-JUN-2002 (rel. 41, Last annotation update)
DE SL cytokine precursor (Fms-related tyrosine kinase 3 ligand) (Flt3
ligand) (Flt3l).
GN FLT3LG.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94195428; PubMed=8145851;
RA Hannum C., Culpepper J., Campbell D., McClanahan T., Zurawski S.,
RA Bazan J.F., Kastelein R., Hudak S., Wagner J., Watson J., Luhn J.,
RA Duda G., Martini N., Peterson D., Menon S., Shanafelt A.,
RA Wuensch M., Kellner G., Nankiwa R., Renick D., Roncero M.G.,
RA Zlotnik A., Rosen O., Dubreuil P., Birnbaum D., Lee F.,
RT Ligand for FLT3/PLK2 receptor tyrosine kinase regulates growth of
RT haematopoietic stem cells and is encoded by variant RNAs.;
RL Nature 368:643-648(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94235842; PubMed=8180375;
RA Lyman S.D., James L., Johnson L., Brasel K., de Vries P.,
RA Escobar S.S., Downey H., Splett R.R., Beckmann M.P., McKenna H.J.,
RT Cloning of the human homologue of the murine flt3 ligand: a growth
RT factor for early hematopoietic progenitor cells.;
RL Blood 83:2795-2801(1994).
RN [3]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RX MEDLINE=96032581; PubMed=7566977;
RA Lyman S.D., Stocking K., Davison B., Fletcher F., Johnson L.,
RA Escobar S.;
RT "Structural analysis of human and murine flt3 ligand genomic loci.";
RL Oncogene 11:1165-1172(1995).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RX MEDLINE=20343011; PubMed=10861197;
RA Savvides S.N., Boone T., Karpus P.A.;
RT "Flt3 ligand structure and unexpected commonalities of helical
RT bundles and cystine knots.";
RL Nat. Struct. Biol. 7:486-491(2000).
CC -1- FUNCTION: STIMULATES THE PROLIFERATION OF EARLY HEMATOPOIETIC
CC CELLS. SYNERGIZES WELL WITH A NUMBER OF OTHER COLOUR STIMULATING
CC FACTORS AND INTERLEUKINS.
CC -1- SUBUNIT: Homodimer (isoform 2).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (isoform 1);
CC secreted (isoform 2).
CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; a 1/membrane-bound (shown here)
CC and 2/soluble; are produced by alternative splicing.

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DR EMBL; U04806; AAA1799.1; -
 DR EMBL; U03858; AAA1825.1; -
 DR EMBL; U29874; AAA90949.1; -
 DR EMBL; U29874; AAA90950.1; -
 DR PDB; 1ETE; 09-JUN-00.
 DR Genew; HENC; 3766; FLT3LG.
 DR MIM; 600007; -
 DR InterPro; IPR004213; FLT3_1lg.
 DR Pfam; PF02947; flt3_1lg; 1.
 KM Cytokine; Glycoprotein; Transmembrane; Alternative splicing; Signal;
 KM 3D-structure; 1
 FT SIGNAL 1 26
 FT CHAIN 27 235
 FT DOMAIN 27 184
 FT TRANSMEM 185 205
 FT DOMAIN 206 235
 FT DISULFID 30 111
 FT DISULFID 70 153
 FT DISULFID 119 158
 FT CARBOHYD 126 149
 FT CARBOHYD 149 178
 FT VARSPPLIC 161 178
 FT FT
 FT VARSPPLIC 179 235
 FT CONFLICT 72 72
 FT SEQUNCE 235 AA; 26416 MW; 73895BF693B4CCEFCRC64;
 Query Match 100.0%; Score 1242; DR 1; Length 235;
 Best Local Similarity 100.0%; Pred. No. 1.1e-96;
 Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MVLAPAMSPPTLYLLLLLSGLSGTQDSCFQHSPISSDFAVKIRELSYLLQDYVTV 60
 DB 1 MVLAPAMSPPTLYLLLLLSGLSGTQDSCFQHSPISSDFAVKIRELSYLLQDYVTV 60
 QY 61 ASNLQDELCGGIMRLVLAQRMERLKTVAAGSKMGLLEVENTEIHFTVTCARQPPESC 120
 DB 61 ASNLQDELCGGIMRLVLAQRMERLKTVAAGSKMGLLEVENTEIHFTVTCARQPPESC 120
 QY 121 RFVQTNISRLLOETSEDLVAKPMTNRONSRLCLEOCOPDSSTLPPMSPRPLEATAPT 180
 DB 121 RFVQTNISRLLOETSEDLVAKPMTNRONSRLCLEOCOPDSSTLPPMSPRPLEATAPT 180
 QY 181 APQPPILLLLLVGILLAAAMCLHMORTRRTPRPGEOVPVPSQDILLVEH 235
 DB 181 APQPPILLLLLVGILLAAAMCLHMORTRRTPRPGEOVPVPSQDILLVEH 235
 RESULT 2
 ID FL3L_MOUSE STANDARD; PRT; 232 AA.
 AC P49772; 064085;
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE SL cytokine precursor (fms-related tyrosine kinase 3 ligand) (FLT3
 DE ligand) (Flt3l).
 GN FLT3LG OR FLT3L.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC NCBI_TaxID:10090;
 CC [1]
 CC SEQUENCE FROM N.A.
 CC MEDLINE-94195428; PubMed-8145851;
 RX

RA Hannum C., Culpepper J., Campbell D., McClanahan T., Zurawski S.,
 RA Bazar J.F., Kastlein R., Hudak S., Wagner J., Mattson J., Luh J.,
 RA Duda G., Martina N., Peterson D., Menon S., Shanfield A.,
 RA Muench M., Kellner G., Nankawa R., Kennick D., Roncarolo M.G.,
 RA Zlotnik A., Rosnet O., Dubreuil P., Birnbaum D., Lee F.,
 RA "Ligand for FLT3/FLK2 receptor tyrosine kinase regulates growth of
 RA hematopoietic stem cells and is encoded by variant RNAs."
 RL Nature 368:643-648(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SUL/J.
 RX MEDLINE-94084791; PubMed-7505204;
 RA Lyman S.D., James L., Vandenbos T., Devries P., Brasel K.,
 RA Gliniak B., Hollingsworth L.T., Picha K.S., McKenna H.J.,
 RA Spletter R.R., Fletcher F.A., Maraskovsky E., Farran T.,
 RA Foxworth D., Williams D.E., Beckmann M.P.,
 RA "Molecular cloning of a ligand for the flt3/flt-2 tyrosine kinase
 RA receptor: a proliferative factor for primitive hematopoietic cells."
 RL Cell 75:1157-1167(1993).
 RN [3]
 RP SEQUENCE FROM N.A. AND ALTERNATIVE SPLICING.
 RX MEDLINE-96032581; PubMed-7566977;
 RA Lyman S.D., Stocking K., Davison B., Fletcher F., Johnson L.,
 RA Escobar S.,
 RA "Structural analysis of human and murine flt3 ligand genomic loci."
 RL Oncogene 11:1165-1172(1995).
 RN [4]
 RP SEQUENCE FROM N.A. AND ALTERNATIVE SPLICING.
 RX MEDLINE-95124710; PubMed-7824267;
 RA Lyman S.D., James L., Escobar S., Downey H., de Vries P.,
 RA Brasel K., Stocking K., Beckmann M.P., Copeland N.G.,
 RA Cleveland L.S.,
 RA "Identification of soluble and membrane-bound isoforms of the murine
 RA flt3 ligand generated by alternative splicing of mRNAs."
 RL Oncogene 10:149-157(1995).
 RN [5]
 RP SEQUENCE FROM N.A.
 RA McClanahan T., Culpepper J., Campbell D., Wagner J.,
 RA Franz-Bacon K., Mattson J., Tsai S., Luh J., Guimares M.J.,
 RA Mettel M.-G., Rosnet O., Birnbaum D., Hannum C.,
 RL Submitted (Apr-1996) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: STIMULATES THE PROLIFERATION OF EARLY HEMATOPOIETIC
 CC CELLS. SYNERGIZES WELL WITH A NUMBER OF OTHER COLONY STIMULATING
 CC FACTORS AND INTERLEUKINS.
 CC -1- SUBUNIT: Homodimer (soluble isoform) (By similarity).
 CC -1- isoforms are also produced by alternative splicing. One of which,
 CC isoform 3/E6, is biologically active, while the other, isoform
 CC 4/E6delta16, is inactive.
 CC -1- ALTERNATIVE PRODUCTS: 4 isoforms; 1/6C (shown here), 2/5H, 3/E6
 CC and 4/E6delta16; are produced by alternative splicing
 CC -----
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CC TISSUE-Fetal brain; PubMed-10087195;
 RX MEDLINE-99189236; PubMed-10087195;
 RA Ng G.Y.K., McDonald T., Bonnett T., Rigby M., Heavens R., Whiting P.,
 RA Chateauf A., Coulombe N., Kargman S., Caskey T., Evans J.F.,
 RA O'Neill G.P., Liu Q.;
 RT Cloning of a novel G-protein-coupled receptor GPR 51 resembling GABAB
 RT receptors expressed predominantly in nervous tissues and mapped
 RT proximal to the hereditary sensory neuropathy type 1 locus on
 RT chromosome 9.";
 RL Genomics 56:288-295(1999).
 RN [6].
 RP SEQUENCE FROM N.A. (ISOFORM 2A), AND VARIANTS PHE-628 AND ALA-869.
 RC TISSUE-Brain;
 RX MEDLINE-99263199; PubMed-10328880;
 RA Martin S.C., Russek S.J., Farb D.H.,
 RT Molecular identification of the human GABABR2: cell surface
 RT expression and coupling to adenylyl cyclase in the absence of
 RT GABABR1.";
 RL Mol. Cell. Neurosci. 13:180-191(1999).
 RN [7].
 RP R1A-R2 INTERACTION.
 RX MEDLINE-99175124; PubMed-10075644;
 RA Ng G.Y.K., Clark J., Coulombe N., Ethier N., Hebert T.E., Sullivan R.,
 RA Kargman S., Chateauf A., Tsukamoto N., McDonald T., Whiting P.,
 RA Mezey E., Johnson M.P., Liu Q., Kolakowski L.F. Jr., Evans J.F.,
 RA Bonner T.I., O'Neill G.P.;
 RT Identification of a GABAB receptor subunit, gb2, required for
 RT functional GABAB receptor activity.";
 RL J. Biol. Chem. 274:7607-7610(1999).
 RN [8].
 RP R1A-R2 INTERACTION.
 RX MEDLINE-20237752; PubMed-10773016;
 RA Sullivan R., Chateauf A., Coulombe N., Kolakowski L.F. Jr.,
 RA Johnson M.P., Hebert T.E., Ethier N., Belley M., Metters K.,
 RA Abramovitz M., O'Neill G.P., Ng G.Y.K.;
 RT Coexpression of full-length gamma-aminobutyric Acid(B) (GABA(B))
 RT receptors with truncated receptors and metabotropic glutamate
 RT receptor 4 supports the GABA(B) heterodimer as the functional
 RT receptor.";
 RL J. Pharmacol. Exp. Ther. 293:460-467(2000).
 RN [9].
 RP FUNCTION: RECEPTOR FOR GABA. THE ACTIVITY OF THIS RECEPTOR IS
 CC MEDIATED BY G-PROTEINS THAT INHIBITS ADENYLYL CYCLASE ACTIVITY,
 CC STIMULATES PHOSPHOLIPASE A2, ACTIVATES POTASSIUM CHANNELS,
 CC INACTIVATES VOLTAGE-DEPENDENT CALCIUM CHANNELS AND MODULATES
 CC INSULIN PHOSPHOLIPIDS HYDROLYSIS. PLAYS A CRITICAL ROLE IN THE
 CC FINE-TUNING OF INHIBITORY SYNAPTIC TRANSMISSION. PRE-SYNAPTIC
 CC GABA-B-R INHIBIT NEUROTRANSMITTER RELEASE BY DOWN-REGULATING
 CC HIGH-VOLTAGE ACTIVATED CALCIUM CHANNELS, WHEREAS POSTSYNAPTIC
 CC GABA-B-R DECREASE NEURONAL EXCITABILITY BY ACTIVATING A PROMINENT
 CC INWARDLY RECTIFYING POTASSIUM (KIR) CONDUCTANCE THAT UNDERLIES THE
 CC LATE INHIBITORY POSTSYNAPTIC POTENTIALS. NOT ONLY IMPLICATED IN
 CC SYNAPTIC INHIBITION BUT ALSO IN HIPPOCAMPAL LONG-TERM
 CC POTENTIATION, SLOW WAVE SLEEP, MUSCLE RELAXATION AND
 CC ANTI-NOCEPTION.
 CC [10].
 CC SUBUNIT: HETERO-DIMER OF GABA-B-R1 AND GABA-B-R2. NEITHER OF WHICH
 CC IS EFFECTIVE ON ITS OWN AND HOMODIMERIC ASSEMBLY DOES NOT SEEM TO
 CC HAPPEN.
 CC [11].
 CC SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MOREOVER
 CC COEXPRESSION OF GABA-B-R1 AND GABA-B-R2 APPEARS TO BE A
 CC PREREQUISITE FOR MATURATION AND TRANSPORT OF GABA-B-R1 TO THE
 CC PLASMA MEMBRANE.
 CC [12].
 CC ALTERNATIVE PRODUCTS: 3 ISOFORMS; 2A (SHOWN HERE), 2B AND 2C; ARE
 CC PRODUCED BY ALTERNATIVE SPLICING.
 CC [13].
 CC TISSUE SPECIFICITY: HIGHLY EXPRESSED IN BRAIN, ESPECIALLY IN
 CC CEREBRAL CORTEX, THALAMUS, HIPPOCAMPUS, FRONTAL, OCCIPITAL AND
 CC TEMPORAL LOBE, OCCIPITAL POLE AND CEREBELLUM, FOLLOWED BY CORPUS
 CC CALLOSUM, CAUDATE NUCLEUS, SPINAL CORD, AMYGDALA AND MEDULLA.
 CC [14].
 CC WEAKLY EXPRESSED IN HEART, TESTIS AND SKELETAL MUSCLE.
 CC [15].
 CC [16].
 CC [17].
 CC [18].
 CC [19].
 CC [20].
 CC [21].
 CC [22].
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 CC [58].
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 CC [99].
 CC [100].

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 CC
 CC EMBL: A0102188; CAA09942.1; -
 CC EMBL: AF056085; AAC63228.1; -
 CC EMBL: AF095723; AAC63383.1; -
 CC EMBL: AF095724; AAC63384.1; -
 CC EMBL: AF095784; AAD30389.1; -
 CC EMBL: AF074483; AAD03336.1; -
 CC EMBL: AF069755; AAC99345.1; -
 CC EMBL: AF099033; AAD45867.1; -
 CC Genew: HGNC:4507; GPR51.
 CC InterPro: IPR001828; ANF_receptor.
 CC InterPro: IPR000337; GPCR_Mgr.
 CC Pfam: PF01094; ANF_receptor; 1.
 CC DR Pfam: PF00003; 7tm_3; 1.
 CC DR PROSITE: PS00979; G_PROTEIN_RECP_F3_1; FALSE_NEG.
 CC DR PROSITE: PS00980; G_PROTEIN_RECP_F3_2; FALSE_NEG.
 CC DR PROSITE: PS00981; G_PROTEIN_RECP_F3_3; FALSE_NEG.
 CC DR PROSITE: PS50259; G_PROTEIN_RECP_F3_4; 1.
 CC KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
 CC Postsynaptic membrane; Coiled coil; Alternative splicing;
 CC Polymorphism.
 CC FT SIGNAL 1 41
 CC FT CHAIN 42 941
 CC FT
 CC FT DOMAIN 42 483
 CC FT TRANSMEM 484 504
 CC FT DOMAIN 505 522
 CC FT TRANSMEM 523 543
 CC FT DOMAIN 544 551
 CC FT TRANSMEM 552 572
 CC FT DOMAIN 573 597
 CC FT TRANSMEM 598 618
 CC FT DOMAIN 619 654
 CC FT TRANSMEM 655 675
 CC FT DOMAIN 676 691
 CC FT TRANSMEM 692 712
 CC FT DOMAIN 713 720
 CC FT TRANSMEM 721 741
 CC FT DOMAIN 742 941
 CC FT DOMAIN 781 819
 CC FT CARBOHYD 90 90
 CC FT CARBOHYD 298 298
 CC FT CARBOHYD 389 389
 CC FT CARBOHYD 404 404
 CC FT CARBOHYD 453 453
 CC FT VARSPLIC 902 927
 CC FT VARSPLIC 929 941
 CC FT
 CC FT VARIANT 628 628
 CC FT
 CC FT VARIANT 869 869
 CC FT
 CC FT VARIANT 869 869
 CC FT
 CC FT CONFLICT 6 6
 CC FT CONFLICT 12 12
 CC FT CONFLICT 424 424
 CC FT
 CC SQ SEQUENCE 941 AA: 105821 MW: 09P1773DB0673C5D CRC64:
 CC
 CC Query Match 7.2%; Score 89.5; DB 1; Length 941;
 CC Best Local Similarity 44.1%; Pred. No. 6.4;
 CC Matches 26; Conservative 2; Mismatches 22; Indels 9; Gaps 3;
 CC
 CC 170 SPRLPRLTAPLAPPP-----LILLILLPVGLLLAAMCMLHMRTRRRRRRPGEGVPPV 224
 CC DB 3 SRRSQGPGRPPPPPPPPPPRLILLILLPLPLPLAPGAM--GM--ARKGAPRPPSSPL 56

| RESULT 5 | SGCA_MEANU | STANDARD: | PRT: | 387 AA. |
|----------|--|--|------|--------------------------------------|
| AC | 064253; | | | |
| DT | 16-OCT-2001 (Rel. 40, Created) | | | |
| DT | 16-OCT-2001 (Rel. 40, Last sequence update) | | | |
| DT | 15-JUN-2002 (Rel. 41, Last annotation update) | | | |
| DE | Alpha-sarcoglycan precursor (Alpha-SG) (Adhaliin) (50 kDa dystrophin-associated glycoprotein) (50DaG). | | | |
| DE | SGCA. | | | |
| OS | Mesocricetus auratus (Golden hamster). | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| OC | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae; | | | |
| OC | Mesocricetus. | | | |
| OX | NCBI_TaxID=10036; | | | |
| RP | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RC | STRAIN=Syrian; TISSUE=Heart muscle; | | | |
| RX | MEDLINE=98054328; PubMed=9391120; | | | |
| RA | Sakamoto A., Ono K., Abe M., Jasmijn G., Eki T., Murakami Y., | | | |
| RT | Masaki T., Toyooka T., Hanaka F.; | | | |
| RT | "Both hypertrophic and dilated cardiomyopathies are caused by mutation of the same gene, delta-sarcoglycan, in hamster: an animal model of | | | |
| RT | disrupted dystrophin-associated glycoprotein complex."; | | | |
| RL | Proc. Natl. Acad. Sci. U.S.A. 94:13873-13878(1997). | | | |
| RN | (2) | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RC | STRAIN=F1B; TISSUE=Skeletal muscle; | | | |
| RX | MEDLINE=95278335; PubMed=7758576; | | | |
| RA | Roberts S.L., Campbell K.P.; | | | |
| RT | "Adhaliin mRNA and cDNA sequence are normal in the cardiomyopathic | | | |
| RT | hamster."; | | | |
| RT | FEBS Lett. 364:245-249(1995). | | | |
| CC | -1- FUNCTION: COMPONENT OF THE SARCOGLYCAN COMPLEX, A SUBCOMPLEX OF | | | |
| CC | THE DYSTROPHIN-GLYCOPROTEIN COMPLEX WHICH FORMS A LINK BETWEEN THE | | | |
| CC | F-ACTIN CYTOSKELETON AND THE EXTRACELLULAR MATRIX. | | | |
| CC | -1- SUBCELLULAR LOCATION: Type I membrane protein. Sarcolemmal | | | |
| CC | (Potential). | | | |
| CC | -1- TISSUE SPECIFICITY: STRONGLY EXPRESSED IN SKELETAL AND | | | |
| CC | HEART MUSCLE. | | | |
| CC | -1- SIMILARITY: BELONGS TO THE SARCOGLYCAN ALPHA/EPSILON FAMILY. | | | |
| CC | ----- | | | |
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| CC | use by non-profit institutions as long as its content is in no way | | | |
| CC | modified and this statement is not removed. Usage by and for commercial | | | |
| CC | entities requires a license agreement (see http://www.isb-sib.ch/announce/ | | | |
| CC | or send an email to license@isb-sib.ch). | | | |
| CC | ----- | | | |
| DR | EMBL; D83651; BAA12025.1; - | | | |
| DR | EMBL; U21677; AAA81645.1; - | | | |
| KW | Cytoskeleton; Transmembrane; Glycoprotein; Signal. | | | |
| FT | FT SIGNAL | 1 | 23 | POTENTIAL. |
| FT | CHAIN | 24 | 387 | ALPHA-SARCOGLYCAN. |
| FT | DOMAIN | 24 | 290 | EXTRACELLULAR (POTENTIAL). |
| FT | TRANSMEM | 291 | 311 | POTENTIAL. |
| FT | DOMAIN | 312 | 387 | CYTOPLASMIC (POTENTIAL). |
| FT | DOMAIN | 209 | 335 | CYS-RICH. |
| FT | CARBOHYD | 174 | 174 | N-LINKED (GLCNAc - - -) (POTENTIAL). |
| FT | CARBOHYD | 246 | 246 | N-LINKED (GLCNAc - - -) (POTENTIAL). |
| SO | SEQUENCE | 387 AA; 43326 MW; D855990FAFE646C3F CRC64; | | |

```

Query Match      7.2% Score 89; DB 1; Length 387;
Best Local Similarity 23.4%; Pred. NO.2.6;
Matches 71; Conservative 26; Mismatches 97; Indels 110; Gaps 14;

QY 11 TTYLLLLLSGSGTDCSFQHSPISSDAVKRLRELDYLQDYPYTVASNLDEELC 70
   ||| | : : : : : | | |
Db 115 TTRORLILLI-----EDPGPRLPYGAFLVRSHDVEVL---PSPNAREL-TAL.161
   ||| | : : : : : | | |

QY 71 GGWLRL-----VLAQRMRKLTAVAGSKMOGLLERYNIETIHVT-----K 110
   |||| | : : : : : | | |

```

[illegible]

RA Zhan M., Zhang G., Chisoe S., Murray J., Miller N., Minx P.,
 RA Fulton R., Johnson D., Bemis G., Bentley D., Bradsheaw H., Bourne S.,
 RA Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,
 RA Hinds K., Kemp K., Lettrell P., Layman D., Ozersky P., Rohlfing T.,
 RA Korte T., Walker C., Wamsley A., Woldmann P., Pepin K., Nelson J.,
 RA Emanuel B.S., Shaikh T., Kuranashi H., Saita S., Budarf M.L.,
 RA McDaniel H.E., Johnson A., Wong A.C.C., Morrow B.E., Edelmann L.,
 RA Kim U.J., Shiyu H., Simon M.I., Dumasht J.P., Peyrard M., Kedra D.,
 RA Serousi E., Franssen I., Tapia I., Bruder C.E., O'Brien K.P.,
 RA Wilkinson P., Bodenteich A., Hartman K., Hu X., Khan A.S., Lane L.,
 RA Tilahun Y., Wright H.,
 RT The DNA sequence of human chromosome 22."
 RL Nature 402:489-495(1999).
 [3]
 RP CHARACTERIZATION OF THE SPLICING FACTOR SF3A REQUIRED FOR 'A'
 RX MEDLINE:20337962; PubMed:10882114;
 RT MEDLINE:20337962; PubMed:10882114;
 RT Functional association of U2 snRNP with the ATP-independent
 RT spliceosomal complex E."
 RL Mol. Cell 5:779-787(2000).
 CC -1- FUNCTION: SUBUNIT OF THE SPLICING FACTOR SF3A REQUIRED FOR 'A'
 CC COMPLEX ASSEMBLY FORMED BY THE STABLE BINDING OF U2 SNRNP TO THE
 CC BRANCHPOINT SEQUENCE (BPS) IN PRE-MRNA. SEQUENCE INDEPENDENT
 CC BINDING OF SF3A/SF3B COMPLEX UPSTREAM OF THE BRANCH SITE IS
 CC ESSENTIAL. IT MAY ANCHOR U2 SNRNP TO THE PRE-MRNA. MAY ALSO BE
 CC INVOLVED IN THE ASSEMBLY OF THE 'E' COMPLEX.
 CC -1- SUBUNIT: COMPONENT OF SPLICING FACTOR SF3A WHICH IS COMPOSED OF
 CC THREE SUBUNITS: SF3A3/SAP61, SF3A2/SAP62, SF3A1/SAP14. SF3A
 CC ASSOCIATES WITH THE SPLICING FACTOR SF3B AND A 12S RNA UNIT TO
 CC FORM THE U2 SMALL NUCLEAR RIBONUCLEOPROTEIN COMPLEX (U2 SNRNP).
 CC INTERACTS WITH SF3A3.
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -1- TISSUE SPECIFICITY: UBIQUITOUSLY EXPRESSED.
 CC -1- SIMILARITY: CONTAINS 1 UBIQUITIN-LIKE DOMAIN.
 CC -1- SIMILARITY: TO YEAST PRE-MRNA SPLICING FACTOR PRP21.
 CC -----
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 CC -----
 DR EMBL: X85237; CAA59494.1; -
 DR EMBL: AC004997; AAC23435.1; -
 DR HSP: 015843; IND.
 DR GeneW: HGNC:10765; SF3A1.
 DR MIM: 605395; -
 DR InterPro: IPR000061; Surp.
 DR InterPro: IPR000626; Ubiquitin.
 DR Pfam: PF00240; ubiquitin.1.
 DR Pfam: PF01805; Surp. 2.
 DR SMART: SM00213; UBO.1.
 DR PROSITE: PS50053; UBIQUITIN_2.1.
 DR KMW: SUBCELLULAR LOCATION: mRNA processing; Nuclear protein; Repeat.
 RT REPEAT 52 94
 FT REPEAT 166 208 SURP MOTIF 1.
 FT REPEAT 707 793 UBIQUITIN-LIKE.
 FT DOMAIN 10 16 POLY-PRO.
 FT DOMAIN 118 122 POLY-GLN.
 FT DOMAIN 260 267 POLY-GLU.
 FT DOMAIN 369 372 POLY-PRO.
 FT DOMAIN 557 560 POLY-PRO.
 FT DOMAIN 672 675 POLY-PRO.
 SO SEQUENCE 793 AA; 88886 MM; 7259PBC4577305C CRC64;
 Query Match 7.2%; Score 89; DB 1; Length 793;
 Best Local Similarity 22.3%; Pred. No. 5.8;
 Matches 67; Conservative 34; Mismatches 79; Indels 120; Gaps 17;

DB 401 LPPAPAPDEXLV-----SPITGE--KI-----PAGK 424
 QY 64 LQDEELCGGIMRLVLAQRNME-RLKTV-----AGSKQGLLRNNTITLF 107
 DB 425 MOEHMRIG-----LLPRWLEQRDRSIREKQSDDEVYAPGLDISSLSKOLAER-RTDIFG 478
 QY 108 VTRCA-----POPPSCLERF-----VOTNISRLQETSGLVALPWI 145
 DB 479 VETATGKRTGEEELQKPEEKVWDGSGSMARQQAQANIT--LQDQLEAIHKAGLV 536
 QY 146 ---TRQNF---SRCLELQCP-----DSSLTLP-----PWSBRPLEAT---APT 180
 DB 537 PEDOTEKIKGSKPNEIPQPPSSATNIPSSAPITSVPRPTMPPTVAVSAVPV 596
 QY 181 APPPLLLLLLVGLLLAANCLHWQR-----RRPRGEOVPP---VSP 227
 DB 597 MPRPPASVVRLPFGSVIAPMPPIIHAPRINVVMPSPAPPIAPRPPMIVPFAVPAP 656
 RESULT 7
 TNR3_MOUSE
 ID TNR3_MOUSE STANDARD; PRT; 415 AA.
 AC P50284;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 3 precursor
 DE (Lymphotoxin-beta receptor).
 GN LTBR OR TNFRSF3 OR TNFCR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathu; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CVB; TISSUE-Lung;
 RX MEDLINE:96072804; PubMed:7594541;
 RA Force W.R., Walter B.N., Hession C., Tizard R., Kozak C.A.,
 RA Browning J.L., Ware C.F.,
 RT "Mouse lymphotoxin-beta receptor. Molecular genetics, ligand binding,
 RT and expression."
 RL J. Immunol. 155:5280-5288(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE:96163885; PubMed-8586432;
 RA Nakamura T., Tashiro K., Nakazawa M., Nakano T., Sasayama S.,
 RT Honjo T.;
 RT "The murine lymphotoxin-beta receptor cDNA: Isolation by the signal
 RT sequence trap and chromosomal mapping."
 RL Genomics 30:312-319(1995).
 CC -1- FUNCTION: Receptor for the heterotrimeric lymphotoxin containing
 CC LTA and LTB, and for TNFSF4/LIGHT. Promotes apoptosis via TRAF3
 CC and TRAF5. May play a role in the development of lymphoid organs
 CC (By similarity).
 CC -1- SUBUNIT: Self-associates (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
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 CC -----
 DR EMBL: U29173; AAA68964.1; -
 DR EMBL: L38423; AAB00846.1; -
 DR EMBL: U30798; AAB1334.1; -
 DR HSP: 014763; IDOG.
 DR MGD: MGI:104875; Ltbr.
 DR InterPro: IPR001368; TNFR_C6.

DR Pfam: PF00020; TNFR_C6; 3.
 DR ProDom: PD000771; TNFR_C6; 1.
 DR SMART: SM00208; TNFR; 3.
 DR PROSITE: PS00652; TNFR_NGFR_1; 2.
 DR PROSITE: PS50050; TNFR_NGFR_2; 3.
 KW Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
 FT SIGNAL 1 30
 FT CHAIN 31 415
 FT DOMAIN 31 223
 FT TRANSMEM 224 244
 FT DOMAIN 245 415
 FT REPEAT 42 81
 FT REPEAT 82 124
 FT REPEAT 125 170
 FT REPEAT 171 213
 FT DISULFID 43 58
 FT DISULFID 59 72
 FT DISULFID 62 80
 FT DISULFID 83 98
 FT DISULFID 101 116
 FT DISULFID 124 132
 FT DISULFID 139 150
 FT DISULFID 142 169
 FT DISULFID 172 187
 FT CARBOHYD 40 40
 FT CARBOHYD 179 179
 SQ SEQUENCE 415 AA; 44956 MW; 29B326A56AE661 CRC64;
 Query Match 7.08; Score 87.5; DB 1; Length 415;
 Best Local Similarity 24.48; Pred. No. 3.7;
 Matches 39; Conservative 20; Mismatches 52; Indels 49; Gaps 8;
 QY 110 KCARPPSPSC-----RPV-----QTISRLQTSSEQLVAKWITRONS 151
 DB 123 ECRQPGMSCYLDNECVCEERLYLQCPGTEAEVDIMOTDNCVCPCKGHQNTSS 182
 QY 152 RCLRLQCPDSSLTLPWPSPPLLENTAP-----TAQPPILLILLVPGILL--- 198
 DB 183 P-RARQCPHTRC-----EIGGVLAAGCTSYSDTICKNPFGAMLLAILSLVFL 235
 QY 199 -----LAAWCLHWQRT-----RRTPPGSGQVPPVSPQ 228
 DB 236 FTVLACAMRHPSLCKRLGTLTKRHPE-GEESPCCAPAR 274
 RESULT 8
 MPT_DROME STANDARD; PRT; 479 AA.
 AC P20483; Q9VAL9;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE M-phase inducer phosphatase (EC 3.1.3.48) (String protein) (Cdc25-like protein)
 GN STG OR CDC25 OR CGI395.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89195217; PubMed=2702688;
 RA Edgar B.A., O'Farrell P.H.;
 RT "Genetic control of cell division patterns in the Drosophila embryo";
 RL Cell 57:177-187(1989).
 RN (2)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91006056; PubMed=2120044;
 RA Jimenez J., Alphey L., Nurse P., Glover D.M.;
 RT "Complementation of fission yeast cdc25s and cdc25ts mutants

RT identifies two cell cycle genes from Drosophila: a cdc2 homologue and
 RT string ".
 RL EMBL J. 9:3565-3571(1990).
 RN (3)
 RP SEQUENCE FROM N.A.
 RC STRAIN=berkeley;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gccayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,
 RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Milos G.L.G.,
 RA Abril J.F., Aoyagi A., An H.-J., Andrews-Frankoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bertram B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foslter C., Gabriellian A.E., Gary N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegam C.,
 RA Jatali M., Kalush F., Kapten G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodika C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laszko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merulov G., Mishina N.V., Mobarry C., Morris J., Mostreli A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusslein D.R., Paclet J.M.,
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svrtskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveril J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster";
 RL Science 287:2185-2195(2000).
 CC -I- FUNCTION: THIS PROTEIN FUNCTIONS AS A DOSAGE-DEPENDENT INDUCER IN
 CC MITOTIC CONTROL. IT IS A TYROSINE PROTEIN PHOSPHATASE REQUIRED FOR
 CC PROGRESSION OF THE CELL CYCLE. IT MAY DIRECTLY DEPHOSPHORYLATE
 CC P34(CDC2) AND ACTIVATE THE P34(CDC2) KINASE ACTIVITY.
 CC -I- CATALYTIC ACTIVITY: protein tyrosine phosphatase + H(2)O = protein
 CC tyrosine + phosphate.
 CC -I- SIMILARITY: BELONGS TO THE MPT PHOSPHATASE FAMILY.
 CC -I- SIMILARITY: CONTAINS 1 RHODANESE DOMAIN.
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 CC -----
 CC EMBL: M24909; AAA28916.1; -
 CC EMBL: X57495; CAA40732.1; -
 CC EMBL: AE003768; AAF56885.1; -
 CC PIR: A32290; A32290.
 CC PIR: S12008; S12008.
 CC HSSP: P30304; 1C25.
 CC Flybase: FBgn0003525; stg.
 CC InterPro: IPR000751; MPT_Phosphatase.
 CC InterPro: IPR001763; Rhodanese-like.
 CC Pfam: PF00581; Rhodanese; 1.
 CC PRINTS: PR00716; MPTPHPTASE.

DR SMART; SM00450; RHOD. 1.
 KW Cell division; Mitosis; Hydrolase.
 FT DOMAIN 319 430 RHODANESE.
 FT ACT_SITE 379 379 BY SIMILARITY.
 FT CONFLICT 228 228 A -> T (IN REF. 1)
 SQ SEQUENCE 479 AA; 54094 MW; 68483f3a285962cc CRC64;

Query Match 7.0%; Score 87.5; DB 1; Length 479;
 Best Local Similarity 22.9%; Pred. No. 4.4;
 Matches 56; Conservative 34; Mismatches 76; Indels 79; Gaps 14;

QY 1 MYVLAPAMPTTYLL---LLLSGLSTOCSPHSHISSDPVAVKIELSDYLDY 57
 DB 72 MLLSPGSPQFQIVROPKIIPANGVSS-----DHTRPARS-FRI-FNLSLS-----T 117
 QY 58 VIVASNIODEELGGLMLRVLQRMWRERLKVAGSKMGLLEVNTEHFVVKCARQPP 117
 DB 118 CMESMSMDE-----IMELFEMSOSO-----QTALCF-----P 146
 QY 118 SCLRFVQINISRLQETSEQLVALRP---WTRONFSRCLEF--OCOPDSSTLPPWSPRP 173
 DB 147 SGLN-----SLISQIIEQPAKSPAGLSMRSPSVRCLSTMTESNTSTTPPKTPE- 199
 QY 174 LEATAPTA---POPULLLLLPVGLLLLAAMCLHMOTRRTRPRPGQVPPVSPDL 230
 DB 200 ---TARDCKRPEP-----ASANCSPDIOSKRHRCAVEKENCAPAPLSQ 242
 QY 231 LLYEH 235
 DB 243 VTISH 247

RESULT 9
 DDRL_RAT STANDARD: PRT; 910 AA.
 AC 063474;
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Epithelial discoidin domain receptor 1 precursor (EC 2.7.1.112)
 DE (Tyrosine-protein kinase CAK) (Cell adhesion kinase) (Tyrosine kinase
 DE DDR) (Discoidin receptor tyrosine kinase) (Protein-tyrosine kinase
 DE PTK-3).
 GN DDRL OR EDDRL OR PTK3.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 OC NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Brain;
 RA MEDLINE=94173920; PubMed=8127887;
 RA Sanchez M.P., Tapley P., Saini S.S., He B., Pulido D., Barbacid M.;
 RT "Multiple tyrosine protein kinases in rat hippocampal neurons: Isolation of ptk-3, a receptor expressed in proliferative zones of the developing brain.";
 RT Proc. Natl. Acad. Sci. U.S.A. 91:1819-1823(1994).
 RL -1- FUNCTION: MAY BE INVOLVED IN CELL-CELL INTERACTIONS AND RECOGNITION (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine -> ADP + protein tyrosine phosphate.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: VARIOUS EMBRYONIC AND ADULT TISSUES; ALSO PROLIFERATIVE ZONES OF THE DEVELOPING BRAIN; HIPPOCAMPAL NEURONS.
 CC -1- SIMILARITY: WITH THE CONSERVED CATALYTIC DOMAINS OF TYR-PROTEIN KINASES.
 CC -1- SIMILARITY: CONTAINS 1 F5/8 TYPE C DOMAIN.
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. INSULIN RECEPTOR SUBFAMILY.
 CC -----
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 CC or send an email to license@isb.slb.ch.)
 CC -----
 CC EMBL; I26525; AAA21089.1; -
 DR HSSP; P00523; 2PTK.
 DR InterPro: IPR000719; Euk_PKinase.
 DR InterPro: IPR000421; FA58_C.
 DR InterPro: IPR002011; RTKinaseII.
 DR InterPro: IPR001245; Tyr_PKinase.
 DR Pfam; PF00754; F5_F8_type-C; 1.
 DR ProDom; PD000001; Euk_PKinase; 1.
 DR SMART; SM00231; FA58C; 1.
 DR SMART; SM00219; TYRK; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS00239; RECEPTOR_TYR_KIN_II; 1.
 DR PROSITE; PS01285; FA58C_1; 1.
 DR PROSITE; PS01286; FA58C_2; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 KW Phosphorylation; Tyrosine-protein kinase; Glycoprotein; Signal;
 FT SIGNAL 1
 FT CHAIN 20 910
 FT DOMAIN 20 413
 FT TRANSMEM 414 440
 FT DOMAIN 441 910
 FT DOMAIN 32 186
 FT DOMAIN 378 412
 FT DOMAIN 473 598
 FT DOMAIN 607 902
 FT NP_BIND 613 621
 FT BINDING 652 652
 FT ACT_SITE 763 763
 FT DISULFID 32 186
 FT MOD_RES 510 510
 FT MOD_RES 789 789
 FT MOD_RES 793 793
 FT MOD_RES 794 794
 FT CARBOHYD 212 212
 FT CARBOHYD 261 261
 FT CARBOHYD 371 371
 FT CARBOHYD 391 391
 SQ SEQUENCE 910 AA; 101164 MW; 7E7FFA1DC8029806 CRC64;

Query Match 7.0%; Score 87; DB 1; Length 910;
 Best Local Similarity 24.5%; Pred. No. 10;
 Matches 38; Conservative 12; Mismatches 35; Indels 70; Gaps 9;

QY 143 PTTTRNFNSRCLELQOQPOSTLP-PW-----SPRPLEATA-----PTAPQP----- 184
 DB 356 PWLSEISFISDV-VNDSDTFPPAPWPPGPPTFSSLELEPRGQPVANAAGSPTA 414
 QY 185 -----PLLLLLPVLGILLLAAMCLHMOR-----TRRR-----T 214
 DB 415 ILIGCAVAILLLLLIALLML-----WRLHRRLLSKAERVALEELVHLSVPGDITLIN 470
 QY 215 PRPGQVPP-----VSPQDILL 232
 DB 471 NRPGRPEPPYOEPFRPGTPTHSAPCVNPGSALLL 505

RESULT 10
 DDRL_MOUSE STANDARD: PRT; 911 AA.
 AC 003146;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Epithelial discoidin domain receptor 1 precursor (EC 2.7.1.112)
 DE (Tyrosine-protein kinase CAK) (Cell adhesion kinase) (Tyrosine kinase

DE DDB (Discoïdin receptor tyrosine kinase) (Protein-tyrosine kinase
 DE MPR-6).
 GN DDB1 OR EDD1 OR CAK OR MPR6.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 RC STRAIN=C57BL/6;
 RX MEDLINE=96204002; PubMed=8622863;
 RA Perez J.L., Jing S.Q., Wong T.W.;
 RT "Identification of two isoforms of the Cak receptor kinase that are
 RT coexpressed in breast tumor cell lines."
 RL Oncogene 12:1469-1477(1996).
 RN [2]
 RP SEQUENCE OF 766-822 FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Embryonic brain;
 RX MEDLINE=93056484; PubMed=1281307;
 RA Gialardi-Hebenstreit P., Nieto M.A., Frain M., Mattei M.-G.,
 RA Chastler A., Wilkinson D.G., Charney P.;
 RT "An Eph-related receptor protein tyrosine kinase gene segmentally
 RT expressed in the developing mouse hindbrain."
 RL Oncogene 7:2499-2506(1992).
 CC -1- FUNCTION: MAY BE INVOLVED IN CELL-CELL INTERACTIONS AND
 CC RECOGNITION (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine -> ADP + protein
 CC tyrosine phosphate.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; CAK I (SHOWN HERE) AND CAK II;
 CC ARE PRODUCED BY ALTERNATIVE SPLICING. THEY ONLY DIFFER BY THE
 CC ABSENCE OF A 37 RESIDUES SEGMENT.
 CC -1- TISSUE SPECIFICITY: THE PREDOMINANT ISOFORM CAK I, IS EXPRESSED IN
 CC DEVELOPING EMBRYO AND ADULT BRAIN; CAK II IS EXPRESSED IN VARIOUS
 CC EPITHELIAL CELLS.
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. INSULIN
 CC RECEPTOR SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 FS/8 TYPE C DOMAIN.
 CC -----
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 CC -----
 DR EMBL: L57509; AAB05209.1; -;
 DR EMBL: X57240; CAA0516.1; -;
 DR PIR: S30502; S30502.
 DR HSSP: P00523; PTK.
 DR MGD: MGI:99216; Pdk1.
 DR DR: IPR000719; Euk_Pkinase.
 DR InterPro: IPR000421; PASE_C.
 DR InterPro: IPR002011; RTKinaseIT.
 DR InterPro: IPR001245; Tyr_Pkinase.
 DR Pfam: PF00069; Pkinase.1.
 DR Pfam: PF00754; F5_F8_TypeC.1.
 DR ProDom: PD000001; Euk_Pkinase.1.
 DR SMART: SM00231; PASEC.1.
 DR SMART: SM00219; TYRC.1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ARP; FALSE_NEG.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR.1.
 DR PROSITE: PS00111; PROTEIN_KINASE_DOM.1.
 DR PROSITE: PS00239; RECEPTOR_TYR_KIN_II.1.
 DR PROSITE: PS01285; PASEC.1.
 DR PROSITE: PS01286; PASEC.2.1.
 DR Transferrase: Tyrosine-protein kinase; Glycoprotein; Signal;
 KW Phosphorylation; Transmembrane; Receptor; ATP-binding;
 KW Alternative splicing.
 FT SIGNAL 1 19 POTENTIAL.
 FT CHAIN 20 911 EPITHELIAL DISCOIDIN DOMAIN RECEPTOR 1.
 FT DOMAIN 20 414 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 415 441 POTENTIAL.
 FT DOMAIN 442 911 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 32 186 FS/8 TYPE C (PHOSPHOLIPID-BINDING,
 FT POTENTIAL).
 FT DOMAIN 379 413 GLY/PRO-RICH.
 FT DOMAIN 474 599 GLY/PRO-RICH.
 FT NP_BIND 608 903 PROTEIN KINASE.
 FT BINDING 614 622 ATP (BY SIMILARITY).
 FT ACT_SITE 653 653 ATP (BY SIMILARITY).
 FT ACT_SITE 764 764 BY SIMILARITY.
 FT MOD_RES 32 186 BY SIMILARITY.
 FT MOD_RES 511 511 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT MOD_RES 790 790 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT MOD_RES 794 794 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT MOD_RES 795 795 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT CARBOHYD 213 213 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 372 372 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPPLIC 503 539 MISSING (IN ISOFORM CAK II).
 SQ SEQUENCE 911 AA; 101160 MW; DBB7FE03DD79510 CMC64;
 Query Match 7.0%; Score 87; DB 1; Length 911;
 Best Local Similarity 24.5%; Pred. No. 10;
 Matches 38; Conservative 12; Mismatches 35; Indels 70; Gaps 9;
 QY 143 PITRNONFRCLELOCQPPSSITLP-PW---SPRLEPANA-----PPAPD----- 184
 DB 357 PVLSEIFISDY-VNDSSTFPAPWPPPPPTNFSLELEPRGOQPVAKAGSPRA 415
 QY 185 -----PLLLLLPVGLLLAAMCLHMOR---TRRR-----T 214
 DB 416 ILICGVAIILLILLIALLML-----WRLWRLLSAERVLEELTVHLSVPGDITLLN 471
 QY 215 PRPGQVPP-----VPSPODLL 232
 DB 472 NRPGRPPPPYQEPNRPGRTPPHSAPCPVNGSALLL 506
 RESULT 11
 CNCG4_BOVIN STANDARD; PRT; 1394 AA.
 ID CNCG4_BOVIN Q28181; Q28082; Q03861;
 AC Q28181; Q28082; Q03861;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE 240 kDa protein of rod photoreceptor CNG-channel [contains: Glutamic
 DE acid-rich protein (GARP); Cyclic-nucleotide-gated cation channel 4
 DE (CNG channel 4) (CNG-4) (Cyclic nucleotide-gated cation channel
 DE modulatory subunit)].
 GN CNGB1 OR CNCG4.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RX MEDLINE=96009859; PubMed=7546742;
 RA Goetzes S., Colville C., Mueller F., Dose A., Godde M., Molday L.,
 RA Kaupp U.B., Molday R.S.;
 RT "A 240 kDa protein represents the complete beta subunit of the cyclic
 RT nucleotide-gated channel from rod photoreceptor."
 RL Neuron 15:627-636(1995).
 RN [2]
 RP SEQUENCE OF 454-1394 FROM N.A.
 RC TISSUE-Testis;
 RX MEDLINE=96198098; PubMed=8626431;
 RA Biel M., Zong X., Ludwig A., Sauter A., Hofmann F.;
 RT "Molecular cloning and expression of the modulatory subunit of the
 RT cyclic nucleotide-gated cation channel."
 RL J. Biol. Chem. 271:6349-6355(1996).

DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Cyclic-AMP-dependent transcription factor ATF-5 (Activating
 DE transcription factor 5) (Transcription factor ATF5).
 GN ATF5 OR ATF5.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homalidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-20558615; PubMed-11087824;
 RA White J.H., McIlhinney R.A.J., Wise A., Ciruela F., Chan W.Y.,
 RA Emson P.C., Billington A., Marshall F.H.;
 RT "The GABA_B receptor interacts directly with the related transcription
 RT factors CREB2 and ATF5";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:13967-13972(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Kohroki J., Tanaka K.;
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 161-282 FROM N.A.
 RX MEDLINE-99303793; PubMed-10373550;
 RA Pali D., Meistrich M.L., Pion S.E.;
 RT "Human Cdc34 and Rad6b ubiquitin-conjugating enzymes target repressors
 RT of cyclic AMP-induced transcription for proteolysis";
 RL Mol. Cell. Biol. 19:5001-5013(1999).
 CC -1- FUNCTION: THIS PROTEIN BINDS THE CAMP RESPONSE ELEMENT (CRE)
 CC (CONSENSUS: 5'GTGAGT(A/C)(A/G)-3'), A SEQUENCE PRESENT IN MANY
 CC VIRAL AND CELLULAR PROMOTERS.
 CC -1- SUBUNIT: BINDS DNA AS A DIMER (POTENTIAL). INTERACTS WITH GABAB
 CC RECEPTOR.
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE BZIP FAMILY.
 CC
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 DR EMBL: AF305687; AAC22558.1; -
 DR EMBL: AB021663; BAA78477.2; -
 DR EMBL: AF101388; AAD28370.1; -
 DR TRANSFAC: T04877; -
 DR Genem: HGNC:790; ATF5.
 DR MIM: 606398; -
 DR InterPro: IPR004827; TF_BZIP.
 DR Pfam: PF00170; bZIP.1.
 DR SMART: SM00338; BRU2.1.
 DR PROSITE: PS00036; BZIP_BASIC.1.
 KM Transcription regulation; DNA-binding; Activator; Nuclear protein;
 KM Multigene family.
 FT DOMAIN 123 139 POLY-PRO.
 FT DOMAIN 186 194 POLY-PRO.
 FT DNA_BIND 210 230 BASIC MOTIF.
 FT DOMAIN 236 250 LEUCINE-ZIPPER (PROBABLE).
 FT CONFLICT 161 163 LLA -> RHE (IN REF. 3).
 SO SEQUENCE 282 AA; 30674 MW; DDB2F907CA021550 CAC64;
 Query Match 6.88; Score 85; DB 1; Length 282;
 Best Local Similarity 29.98; Pred. NO. 3.9;
 Matches 38; Conservative 7; Mismatches 38; Indels 44; Gaps 6;
 OY 144 WIT-RONSPRLCLOCQDSTLPPMSPRP--LEATA-----178
 DB 66 WMTERRVDFIALPLPPLPPTLPP--SPTRPDLFAMASLKLKELEQMEDFLDAPPLPP 124
 OY 179 ---PTAPQPLLLLLLPVGL-----LLAAAMCLH--WQTRRRTRPRPGQ 220

DB 125 PSEPPPLPPLPAPSLPLSPFSDLPPQPVLDLFLLLAIYCNNAEQGEVGMPLPPQ 184
 OY 221 VPPVSP 227
 DB 185 QPPPPSP 191
 RESULT 14
 FCGRN_RAT
 ID FCGRN_RAT STANDARD; PRT; 366 AA.
 AC P13599;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE IGG receptor FCGRN large subunit p51 precursor (FCRN) (Neonatal FC
 DE receptor) (IGG FC fragment receptor transporter, alpha chain).
 GN FCGRN OR FCGRN.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RX STRAIN-Miscari;
 RX MEDLINE-89097257; PubMed-2911353;
 RA Stimster N.E., Mostov K.E.;
 RT "An Fc receptor structurally related to MHC class I antigens";
 RL Nature 337:184-187(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Epithelium;
 RX MEDLINE-90315866; PubMed-2534798;
 RA Stimster N.E., Mostov K.E.;
 RT Cloning and expression of the neonatal rat intestinal Fc receptor, a
 RT major histocompatibility complex class I antigen homolog";
 RL Cold Spring Harb. Symp. Quant. Biol. 54:571-580(1989).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
 RX MEDLINE-95059482; PubMed-7969498;
 RA Burneister W.P., Huber A.H., Bjorkman P.J.;
 RT "Crystal structure of the complex of rat neonatal Fc receptor with
 RT Fc";
 RL Nature 372:379-383(1994).
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
 RX MEDLINE-98154319; PubMed-9493268;
 RA Vaughn D.E., Bjorkman P.J.;
 RT "Structural basis of pH-dependent antibody binding by the neonatal Fc
 RT receptor";
 RL Structure 6:63-73(1998).
 CC -1- FUNCTION: BINDS TO THE FC REGION OF MONOMERIC IMMUNOGLOBULINS
 CC GAMMA. MEDIATES THE SELECTIVE UPTAKE OF IGG FROM MILK AND HELPS
 CC NEONORN ANIMALS TO ACQUIRE PASSIVE IMMUNITY. IGG IN THE MILK IS
 CC BOUND AT THE APICAL SURFACE OF THE INTESTINAL EPITHELIUM. THE
 CC RESULTANT FCGRN-IGG COMPLEXES ARE TRANSCYTOSED ACROSS THE
 CC INTESTINAL EPITHELIUM AND IGG IS RELEASED FROM FCGRN INTO BLOOD OR
 CC TISSUE FLUIDS (BY SIMILARITY).
 CC -1- SUBUNIT: FCGRN COMPLEX CONSIST OF TWO SUBUNITS: P51, AND P14 WHICH
 CC IS EQUIVALENT TO BETA-2-MICROGLOBULIN. IT FORMS AN MCH CLASS I -
 CC LIKE HETERODIMER.
 CC -1- TISSUE SPECIFICITY: INTESTINAL EPITHELIUM.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
 CC
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 CC

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|-----------------------|--------|----------------|-------|----------------|
| Query Match | 6.8%; | Score 85; | DB 1; | Length 366; |
| Best Local Similarity | 22.2%; | Pred. No. 5.2; | | |
| Matches | 51; | Conservative | 21; | Mismatches 66; |
| | | | | Indels 92; |
| | | | | Gaps 11 |

"Cloning of the cDNA encoding the mouse ATF1 transcription factor.",
 RL Gene 168:227-231(1996).
 CC -1- FUNCTION: Transcriptional activator that binds to the AT-rich core
 CC sequence of the enhancer element of the AFP gene.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- SIMILARITY: CONTAINS 4 HOMEBOX DOMAINS.

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 DR ENBL; D26046; BAA03046.1; ..
 DR HSSP; P20263; I0CP.
 DR TRANSFAC; T03881; ..
 DR MGD; MG1:99948; Atbfl.
 DR InterPro; IPR001356; Homeobox.
 DR InterPro; IPR000822; Znf.C2H2.
 DR InterPro; IPR003604; Znf.U1.
 DR Pfam; PF00046; homeobox; 4.
 DR Pfam; PF00096; Zf-C2H2; 20.
 DR ProDom; PD000010; Homeobox; 4.
 DR SMART; SM00389; HOX; 4.
 DR SMART; SM00355; Znf.C2H2; 22.
 DR SMART; SM00451; Znf.U1; 7.
 DR PROSITE; PS00027; HOMEBOX_1; 2.
 DR PROSITE; PS00071; HOMEBOX_2; 4.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 15.
 DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 9.
 KW Transcription regulation; Activator; Zinc-finger; Metal-binding;
 KW DNA-binding; Homeobox; Nuclear protein; Repeat.
 FT FT ZN_FING 79 103 C2H2-TYPE.
 FT FT ZN_FING 282 303 C2H2-TYPE.
 FT FT ZN_FING 641 664 C2H2-TYPE.
 FT FT ZN_FING 672 695 C2H2-TYPE.
 FT FT ZN_FING 727 751 C2H2-TYPE.
 FT FT ZN_FING 805 829 C2H2-TYPE (ATYPICAL).
 FT FT ZN_FING 946 969 C2H2-TYPE (DEGENERATE).
 FT FT ZN_FING 985 1009 C2H2-TYPE (ATYPICAL).
 FT FT ZN_FING 1041 1065 C2H2-TYPE (ATYPICAL).
 FT FT ZN_FING 1089 1113 C2H2-TYPE (ATYPICAL).
 FT FT ZN_FING 1233 1256 C2H2-TYPE (ATYPICAL).
 FT FT ZN_FING 1262 1285 C2H2-TYPE (ATYPICAL).
 FT FT ZN_FING 1370 1395 C2H2-TYPE.
 FT FT ZN_FING 1411 1433 C2H2-TYPE.
 FT FT ZN_FING 1439 1462 C2H2-TYPE.
 FT FT ZN_FING 1553 1579 C2H2-TYPE.
 FT FT ZN_FING 1606 1630 C2H2-TYPE.
 FT FT ZN_FING 1990 2013 C2H2-TYPE.
 FT FT DNA_BIND 2152 2211 HOMEBOX 1.
 FT FT DNA_BIND 2249 2308 HOMEBOX 2.
 FT FT ZN_FING 2335 2358 HOMEBOX 3.
 FT FT ZN_FING 2539 2561 C2H2-TYPE.
 FT FT DNA_BIND 2650 2709 HOMEBOX 4.
 FT FT ZN_FING 2720 2743 C2H2-TYPE.
 FT FT DNA_BIND 2952 3011 HOMEBOX 5.
 FT FT ZN_FING 3032 3056 C2H2-TYPE.
 FT FT ZN_FING 3552 3576 C2H2-TYPE.
 FT FT DOMAIN 461 491 POLY-GLU.
 FT FT DOMAIN 771 785 POLY-ALA.
 FT FT DOMAIN 1314 1317 POLY-ALA.
 FT FT DOMAIN 1734 1748 POLY-GLN.
 FT FT DOMAIN 1794 1799 POLY-GLN.
 FT FT DOMAIN 1856 1863 POLY-GLN.
 FT FT DOMAIN 2044 2059 POLY-PRO.
 FT FT DOMAIN 2405 2408 POLY-ALA.
 FT FT DOMAIN 3216 3220 POLY-PRO.
 FT FT DOMAIN 3380 3409 POLY-GLN.
 FT FT DOMAIN 3412 3420 POLY-GLN.
 FT FT DOMAIN 3534 3550 POLY-GLY.

FT DOMAIN 3620 3623 POLY-PRO.
FT DOMAIN 3659 3662 POLY-SER.
SQ SEQUENCE 3726 AA; 406567 MW; 915ACBE58A72C98 CRC64;

Query Match 6.8%; Score 84.5; DB 1; Length 3726;
Best Local Similarity 21.6%; Pred. No. 80; Mismatches 70; Indels 93; Gaps 12;
Matches 53; Conservative 29; Mismatches 70; Indels 93; Gaps 12;

QY 29 DCSFQHSPISSDFAVKIRELSDYLDQYPVTVASNLDEE--LCGGLMRLVLAQRMERL 86
Db 3033 ECTLCGIRKYSARLSVRDHIFSQOHISKVKDTIGSQLDKEXEYFDPATVROLMAGQELDR 3092
QY 87 KTV-----AGSKMOGL-----LERVNTIEHYTKCAFO--PP-----PSCLRFVQTN 126
Db 3093 KKAENVIGLAAQQQGMFDNAPLQALNLP--TTPALQGIIPVLLFGLNRPSPICGFTPAN 3149
QY 127 ISRLQETSEQLVALKPWITRONFSRCLELOCQPDSSITLPPPW-----S 170
Db 3150 TA-----LTSPKP-----NLMLGP-STIVPSGLPTSGLPNKPSASLSS 3188
QY 171 PRPLEATAPTAPOPPPLLLLLLPVGLLLAAAWCLHWQRTRRRTPRPGEQVPP----- 223
Db 3189 PTPAQATWAMAPQP-----PQPQOPQPPVQOPPPPPPAQO 3224
QY 224 VPSPO 228
Db 3225 IPAPQ 3229

Search completed: May 27, 2003, 18:27:34
Job time : 15 secs

GenCore version 5.1.4-P5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 27, 2003, 18:26:11 ; Search time 34 Seconds
(without alignments)
1424.149 Million cell updates/sec

Title: US-08-994-468-6

Perfect score: 1242
Sequence: 1 MVLAPAWSPPTTYLLLLD.....RPGEQVPVPSQDLLLVH 235

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: SP-archaea:*
2: SP-bacteria:*
3: SP-fungi:*
4: SP-human:*
5: SP-invertebrate:*
6: SP-mammal:*
7: SP-mhc:*
8: SP-organella:*
9: SP-phage:*
10: SP-plant:*
11: SP-rodent:*
12: SP-virus:*
13: SP-vertebrate:*
14: SP-unclassified:*
15: SP-rylirus:*
16: SP-bacteriap:*
17: SP-archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1 | 895.5 | 72.1 | 294 | 6 | Q9MZV0 |
| 2 | 894.5 | 72.0 | 291 | 6 | Q9MZU9 |
| 3 | 840 | 67.6 | 292 | 6 | Q9GKE0 |
| 4 | 835 | 67.2 | 292 | 6 | Q9GKE0 |
| 5 | 746 | 60.1 | 274 | 6 | Q8NMW1 |
| 6 | 602.5 | 48.5 | 172 | 11 | Q61K04 |
| 7 | 578 | 46.5 | 169 | 11 | Q8VCH4 |
| 8 | 112.5 | 9.1 | 579 | 10 | Q9L6G8 |
| 9 | 104.5 | 8.4 | 668 | 5 | Q9GY11 |
| 10 | 102.5 | 8.3 | 648 | 5 | Q9GY11 |
| 11 | 100.5 | 8.1 | 1809 | 11 | Q8VIM6 |
| 12 | 98.5 | 7.9 | 345 | 5 | Q9N753 |
| 13 | 95.5 | 7.7 | 1240 | 12 | Q9DMH8 |
| 14 | 93.5 | 7.5 | 658 | 10 | Q9C5T0 |
| 15 | 93 | 7.5 | 1217 | 5 | Q17889 |
| 16 | 92.5 | 7.4 | 387 | 11 | Q8VD70 |

| | | | | | | |
|----|------|-----|------|----|--------|--------------------|
| 17 | 92.5 | 7.4 | 560 | 5 | Q9GYA1 | Q9GYA1 leishmania |
| 18 | 92.5 | 7.4 | 1400 | 5 | Q8SZS7 | Q8SZS7 drosophila |
| 19 | 92 | 7.4 | 251 | 4 | Q9HAD2 | Q9HAD2 homo sapien |
| 20 | 90.5 | 7.3 | 536 | 5 | Q9GYA0 | Q9GYA0 leishmania |
| 21 | 90.5 | 7.3 | 660 | 5 | Q9GY15 | Q9GY15 leishmania |
| 22 | 90.5 | 7.3 | 5120 | 13 | Q9PU36 | Q9PU36 gallus gall |
| 23 | 89.5 | 7.2 | 474 | 5 | Q17610 | Q17610 caenorhabdi |
| 24 | 88.5 | 7.1 | 238 | 16 | Q8YWX3 | Q8YWX3 anabena sp |
| 25 | 88.5 | 7.1 | 270 | 4 | Q9UMT1 | Q9UMT1 homo sapien |
| 26 | 88.5 | 7.1 | 404 | 10 | Q9AMW4 | Q9AMW4 oryza sativ |
| 27 | 88.5 | 7.1 | 1267 | 10 | Q943D5 | Q943D5 oryza sativ |
| 28 | 88.5 | 7.1 | 1386 | 4 | Q75064 | Q75064 homo sapien |
| 29 | 88 | 7.1 | 250 | 6 | Q9GKE2 | Q9GKE2 sus scrofa |
| 30 | 88 | 7.1 | 675 | 11 | Q9DRT2 | Q9DRT2 mus musculu |
| 31 | 88 | 7.1 | 753 | 12 | Q56971 | Q56971 kenneya ye |
| 32 | 87.5 | 7.0 | 470 | 10 | Q9LUI1 | Q9LUI1 arabidopsis |
| 33 | 87.5 | 7.0 | 946 | 10 | Q22015 | Q22015 cylindrothe |
| 34 | 87 | 7.0 | 510 | 5 | Q44018 | Q44018 leishmania |
| 35 | 87 | 7.0 | 5317 | 5 | Q8TA74 | Q8TA74 hemientrot |
| 36 | 86.5 | 7.0 | 299 | 6 | Q9TTT9 | Q9TTT9 bos taurus |
| 37 | 86 | 6.9 | 235 | 11 | Q9D3J3 | Q9D3J3 mus musculu |
| 38 | 86 | 6.9 | 299 | 12 | Q84647 | Q84647 parametium |
| 39 | 86 | 6.9 | 706 | 5 | Q23600 | Q23600 caenorhabdi |
| 40 | 86 | 6.9 | 911 | 11 | Q35407 | Q35407 mus musculu |
| 41 | 85.5 | 6.9 | 795 | 5 | Q95UQ2 | Q95UQ2 toxoplasma |
| 42 | 85 | 6.8 | 282 | 4 | Q9BSA1 | Q9BSA1 homo sapien |
| 43 | 85 | 6.8 | 289 | 16 | Q9A3K1 | Q9A3K1 caulobacter |
| 44 | 85 | 6.8 | 413 | 11 | Q9NMW1 | Q9NMW1 mus musculu |
| 45 | 85 | 6.8 | 1217 | 4 | Q9P2D0 | Q9P2D0 homo sapien |

ALIGNMENTS

RESULT 1

Q9MZV0 PRELIMINARY; PRT; 294 AA.
ID Q9MZV0
AC Q9MZV0
DT 01-OCT-2000 (TREMREL. 15, Created)
DT 01-OCT-2000 (TREMREL. 15, Last sequence update)
DT 01-JUN-2002 (TREMREL. 21, Last annotation update)
DE Flt3 ligand.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20358731; PubMed=10902925;
RA Yang S., Sim G.K.;
RT "Molecular cloning of canine and feline flt3 ligand reveals high
RT degree of similarity to the human and mouse homologue but uniquely
RT long cytoplasmic domain."
RL DNA Seq. 11:163-166(2000).
DR EMBL: AF155148; AAF87088.1;
DR InterPro: IPR004213; Flt3_119.
DR Pfam: PF02947; Flt3_119; 1.
SQ SEQUENCE 294 AA; 32394 MW; 6859917A3B74ABCD CRC64;

Query Match

Best Local Similarity 77.1%; Score 895.5; DB 6; Length 294;
Matches 162; Conservative 12; Mismatches 35; Indels 7; Gaps 3;

| | | | |
|----|-----|---|-----|
| QY | 1 | MTVLAPAWSPPTTYLLLLLSGLSGFQDPSFQSPISDPFAVYIRLSDYLQDYPVY | 60 |
| DB | 1 | MTVLAPAWSPPTTYLLLLLSGLSGFQDPSFQSPISDPFAVYIRLSDYLQDYPVY | 60 |
| QY | 61 | ASNLQDELCCGRLVLAQRMRERLKTAVGSKMGLLEVRNTEHFEVTCAROPPSCL | 120 |
| DB | 61 | ASNLQDELCCGRLVLAQRMRERLKTAVGSKMGLLEVRNTEHFEVTCAROPPSCL | 120 |
| QY | 121 | RFVQTNRSLQETSQVLAALKRWITRQNRSLQLQCCQDSSSTLPPMSRPLEATAPT | 180 |
| DB | 121 | RFVQTNRSLQETSQVLAALKRWITRQNRSLQLQCCQDSSSTLPPMSRPLEATAPT | 180 |

Db 121 RFVQTNISHLLODTSQQALAKPMTITRNFSGCELEOCQSDSSLTVPKPSGALETALP 160

QY 181 APQPP-LTLLTLLPVGILLTAAACLMH-QTRRRTRPPEQVVPVPS-----PQD 229
||| | ||||| ||| : ||||| : ||| : ||| || ||| : |||
Db 181 APQAPRLTLLTLLPVALLMTSTACLMHRRRRRRRSYPSGQRLTRSESHLPED 236

RESULT 2

| | | | | |
|----|---|--------------|------|---------|
| IC | Q9MZU9; | PRELIMINARY; | PTT; | 291 AA. |
| AD | Q9MZU9; | | | |
| DT | 01-OCT-2000 (TrEMBLrel. 15, Created) | | | |
| DT | 01-OCT-2000 (TrEMBLrel. 15, Last sequence update) | | | |
| DT | 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) | | | |
| DE | Fil3 ligand. | | | |
| OS | Felis silvestris catus (Cat). | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| OC | Mammalia; Euthera; Carnivora; Fissipedia; Felidae; Felis. | | | |
| OX | NCBI_TaxID=9685; | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RX | MEDLINE=20358731; PubMed=10902925; | | | |
| RA | Yang S., Sim G.K.; | | | |
| RT | "Molecular cloning of canine and feline fil3 ligand reveals high degree of similarity to the human and mouse homologue but uniquely | | | |
| RT | long cytoplasmic domain." | | | |
| RL | DNA Seq. 11:163-166(2000). | | | |
| DR | EMBL: AF155149; AAF87089.1; - | | | |
| DR | Interpro: IPR004213; FLT3_1lg. | | | |
| DR | Pfam: PF02947; flt3_1lg.1. | | | |
| SO | SEQUENCE 291 AA; 32459 MW; 8F85A10A5EA0DC6 CRC64; | | | |

RESULT 3

| | | | | |
|----|---|---|------|---------|
| ID | 09GKE0 | PRELIMINARY; | PRT; | 292 AA. |
| OC | 09GKE0 | | | |
| DT | 01-MAR-2001 | (TREMBLrel. 16, Created) | | |
| DT | 01-MAR-2001 | (TREMBLrel. 16, last sequence update) | | |
| DT | 01-JDC-2001 | (TREMBLrel. 19, last annotation update) | | |
| DE | P113 ligand isoform-1. | | | |
| OS | Bos taurus (Bovine). | | | |
| OC | Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| OC | Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; | | | |
| OC | Bovidae; Bovinae; Bos. | | | |
| OX | NCBI_TaxID=9913; | | | |
| RP | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RX | MEDLINE=30570936; PubMed=11120823; | | | |
| RA | Hwang J W., Brown W C., Palmer G H.; | | | |
| RT | "Identification of fetal liver tyrosine kinase 3 (P113) ligand domain | | | |
| RT | required for receptor binding and function using naturally occurring | | | |
| RT | ligand isoforms." | | | |
| RT | | | | |

RL J. Immunol., 165:6966-6974(2000).
 DR EMBL, AF229855; AAF99322.1; -
 DR InterPro: IPR004013; Flt3_1lg.
 DR Pfam; PF02947; Flt3_1lg; 1.
 SQ SEQUENCE 292 AA; 32390 MM; D68B9ED7221202D CRC64

RESULT 4

| ID | DBNMW1 | PRELIMINARY; | PRT; | 292 AA. |
|----|---|---|------|---------|
| AC | Q8NMW1 | | | |
| DT | 01-MAR-2002 | (TREMBLrel. 20, Created) | | |
| DT | 01-MAR-2002 | (TREMBLrel. 20, last sequence update) | | |
| DT | 01-JUN-2002 | (TREMBLrel. 21, last annotation update) | | |
| DE | Flt3 ligand. | | | |
| DE | Flt3 ligand. | | | |
| GN | FLT3 LIGAND. | | | |
| OS | Bos taurus (Bovine). | | | |
| OC | Eukaryota; Metazoa; Chordata; Cranialta; Vertebrata; Euta | | | |
| OC | Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora | | | |
| OC | Bovidae; Bovinae; Bos. | | | |
| OX | NCBI_TaxID=9913; | | | |
| RN | {1} | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RA | Hikono H., Momotani E.; | | | |
| RT | "Cloning of a cDNA for bovine flt3 ligand." | | | |
| RL | Submitted (NOV-2000) to the EMBL/Genbank/DBD databases | | | |
| RU | EMBL: AB051841; BAB7634.1; - | | | |
| DR | InterPro: IPR004313; Flt3_lig | | | |
| DR | Pfam: PF02947; flt3_1lig.1 | | | |
| QO | SEQUENCE 292 AA; 32368 MW; 2A797EDC1199C4D9 CRC64; | | | |

RESULT 5

[illegible]

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SQ      SEQUENCE      172 AA: 19465 MW: 04F0A010171E3384 CRC64;

Query Match
Best Local Similarity 48.5%; Score 602.5; DB 11; Length 172;
Matches 122; Conservative 15; Mismatches 28; Indels 3; Gaps 2

QY      1 MTVLAPAMSP-TTYLLLLLLLLSSGSGTDCSFQHSPISSDFAVKIRELSDYLLADYPTV 59
DB      1 MTVLAPAMSPSSILLILLILSPCLRGTPDCYFSHSPISNFKVKRRELIDHLKXKPYT 60
QY      60 VASN0DELCCGGLMPLVLAQRMEKLVVAGSKMOGLERVNTIEHYTKCAFQPPESC 119
DB      61 VAVN0DEKHKKALMSLFLAQRWIEQLKTVAGSKMOTLLEDVNEIHFVTSCTFQPLEC 120
QY      120 LRFVOTNISRLLOETSEQLVALKPWITR--QNFSCLELQCCOPDSSTLP 165
DB      121 LRFVOTNISHLKDTCTQLALKPCIGKACQNFSCLEVQCCOPDRVSL 168

RESULT 7
Q8VCH4 PRELIMINARY: PRT; 169 AA.
AC      O8VCH4:
AC      O8VCH4:
DT      01-MAR-2002 (TREMBLrel. 20, Created)
DT      01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT      01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE      Similar to FMS-like tyrosine kinase 3 ligand.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=LIVER;
RA      Strausberg R.;
RL      Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR      EMBL, BC019801; AAH19801.1;
DR      InterPro: IPR004213; Flt3_119.
PF      Pfam: PF02947; flt3_119; 1.
KW      Kinase.
SQ      SEQUENCE 169 AA: 18986 MW: 5B4CA47D9724EFF2 CRC64;

Query Match
Best Local Similarity 46.5%; Score 578; DB 11; Length 169;
Matches 120; Conservative 14; Mismatches 29; Indels 12; Gaps 3;

QY      1 MTVLAPAMSP-TTYLLLLLLLLSSGSGTDCSFQHSPISSDFAVKIRELSDYLLADYPTV 59
DB      1 MTVLAPAMSPSSILLILLILSPCLRGTPDCYFSHSPISNFKVKRRELIDHLKDYPTV 60
QY      60 VASN0DELCCGGLMPLVLAQRMEKLVVAGSKMOGLERVNTIEHYTKCAFQPPESC 119
DB      61 VAVN0DEKHKKALMSLFLAQRWIEQLKTVAGSKMOTLLEDVNEIHFVTSCTFQPLEC 120
QY      120 LRFVOTNISRLLOETSEQLVALKPWITR--QNFSCLELQCCOPDSSTLP 172
DB      121 LRFVOTNISHLKDTCTQLALKPCIGKACQNFSCLE-----TPPCCPQ 166

RESULT 8
Q9LGG8 PRELIMINARY: PRT; 579 AA.
AC      O9LGG8:
AC      O9LGG8:
DT      01-OCT-2000 (TREMBLrel. 15, Created)
DT      01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT      01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE      Putative extensin-like protein.
GN      P040610.6 OR C01174.D05.5.
OS      Oryza sativa (Rice).
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC      Ehrhartoideae; Oryzeae; Oryza.
OX      NCBI_TaxID=4530;

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SQ SEQUENCE 668 AA; 70725 MW; CEB3ECCAAAC490C94 CRC64;
Query Match 8.4%; Score 104.5; DB 5; Length 668;
Best Local Similarity 26.6%; Pred. No. 0.093;
Matches 63; Conservative 20; Mismatches 77; Indels 77; Gaps 13;
QY 4 LAPANSPPTYLLLLLLSSGSGTDCSFQHSPISSDFAVKIRLESDYLLQDPYTVASN 63
Db 149 LRPENSSMPNLTLOVRLRLKLSGT-----LPADNS-SLKSLSNVNLEDMPT---- 194
QY 64 LQDEELCGGLWRLVLAQRMWERLKTVAAGSKMOGLLERVNTLHFYTKCAFOPPP-----S 118
Db 195 -----GL-----LRPEW-----GSLERIQGLVRLKLTGRLPQPWSPMK 229
QY 119 CLRFVQ--TNISRLQ-----ETSEDVALKP-WITRONFSCLQLQCP 160
Db 230 ALRFELDTGTMISGLTPQWASAVISINLEGTVEGSLTPPEWISMRL-QTLNLRRTK 288
QY 161 DSSRLPPWMSR-----PLEATAPTAQPP-----LLLLLLPVGLL--LAAAW 203
Db 289 VSGTLPEPSSMGSGLANQLSLTGVSGTLPPQWSSMKRLTQLLLDTLLSGTLPAEW 345

RESULT 10
Q9GY33 PRELIMINARY; PRT; 648 AA.
ID Q9GY33
AC Q9GY33;
DT 01-MAR-2001 (TRENBLREL. 16, Created)
DT 01-OCT-2001 (TRENBLREL. 18, Last sequence update)
DE 01-JUN-2002 (TRENBLREL. 21, Last annotation update)
DE Probable surface antigen p2.
GN Lm12.121.
OS Leishmania major.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5664;
RN [1]
RC SEQUENCE FROM N.A.
RP STRAIN=FRIEDELIN;
RA Murphy L., Quail M., Harris D., Rajandream M., Ivens A., Barrell B.,
RA Oliver K.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBAJ databases.
DR EMBL, AL301114, CAC02017.2;-.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR002965; P_f1ch_extensn.
DR Pfam; PF00560; LRR; 7.
DR PRINTS; PRO1217; PRICHEXTENS.
DR SMART; SM00181; EGF_1.
SO SEQUENCE 648 AA; 68470 MW; 8EB78AC101E01286 CRC64;

Query Match 8.3%; Score 102.5; DB 5; Length 648;
Best Local Similarity 26.6%; Pred. No. 0.14;
Matches 63; Conservative 20; Mismatches 77; Indels 77; Gaps 13;
QY 4 LAPANSPPTYLLLLLLSSGSGTDCSFQHSPISSDFAVKIRLESDYLLQDPYTVASN 63
Db 149 LRPENSSMPNLTLOVRLRLKLSGT-----LPADNS-SLKSLSNVNLEDMPT---- 194
QY 64 LQDEELCGGLWRLVLAQRMWERLKTVAAGSKMOGLLERVNTLHFYTKCAFOPPP-----S 118
Db 195 -----GL-----LRPEW-----GSLERIQGLVRLKLTGRLPQPWSPMK 229
QY 119 CLRFVQ--TNISRLQ-----ETSEDVALKP-WITRONFSCLQLQCP 160
Db 230 ALRFELDTGTMISGLTPQWASAVISINLEGTVEGSLTPPEWISMRL-QTLNLRRTK 288
QY 161 DSSRLPPWMSR-----PLEATAPTAQPP-----LLLLLLPVGLL--LAAAW 203
Db 289 VSGTLPEPSSMGSGLANQLSLTGVSGTLPPQWSSMKRLTQLLLDTLLSGTLPAEW 345

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ID 08VIM6 PRELIMINARY; PRT: 1809 AA.
 AC 08VIM6;
 DT 01-MAR-2002 (Tremblrel. 20, Created)
 DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 21, Last annotation update)
 DE Stereocillin.
 GN STRC.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALE/C;
 RX MEDLINE=21547528; PubMed=11687802;
 RA Verpy E., Masmodi S., Zwaenepoel I., Lebovici M., Hutchin T.P.,
 RA Del Castillo I., Nouaille S., Blanchard S., Laine S., Popot J.L.,
 RA Moreno F., Mueller R.F., Petit C.;
 RT "Mutations in a new gene encoding a protein of the hair bundle cause
 RT non-syndromic deafness at the DFNB16 locus."
 RL Nat. Genet. 29:345-349(2001).
 DR EMBL: AF375593; AAL35321.1;
 DR MGD: MGI:2153816; Strc.
 SQ SEQUENCE 1809 AA; 196404 MW; 012382C9E80EC825 CRC64;
 Query Match
 Best Local Similarity 8.1%; Score 100.5; DB 11; Length 1809;
 Matches 70; Conservative 25; Mismatches 93; Indels 107; Gaps 14;
 QY 3 VLAPASPTTYLL-----LLLL-----SSGLSGQDCSFQHSPISSDPAVKIRE 47
 DB 168 VLADLPLSLMLLEGTMOALVOLQPSVDPINATGLDG-----RE 208
 QY 48 LSDYLLQDY--PYTVASNLQDEE-LCGLMRLV---LAQRMERLKV----- 89
 DB 209 PAHPLQGLLITPAGELGSESEALNGLLRTYGAPLYAFOGELLRVTHSLQDEVSIM 268
 QY 90 -----AGSKMGLLEVRNTEIHFVTKC-----AFQPPSCLRFVQNTISRL 131
 DB 269 GQEPDASGCGGNGLOQLLMQMRNNLSMDARALGFLSGSPPPRLNCLSGV--L 326
 QY 132 QETSEDLVAKWITRONSRCLLQCCPDSSILPP-----PWSPPLE 175
 DB 327 PRASQPAHISP--RQRAISVEALCENHSGPEPYSISFISYLLQHIKIPATPPPP 383
 QY 176 AT---APTAPOPPLLLLLLPVGLLLLAAMCLHMQRTRRRPRGQV--PPPS 226
 DB 384 TTPRPPTTPQPPPTTTPPTTTP-----DTTQPPVPTPRPPPTTPQPPPS 426
 RESULT 12
 Q9N753
 ID 09N753 PRELIMINARY; PRT: 345 AA.
 AC 09N753;
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2001 (Tremblrel. 18, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE Probable surface antigen p2.
 GN IM2.08.
 OS Leishmania major.
 OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
 OC NCBI_TaxID=5664;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FRIEDLIN;
 RA Murphy L., Quail M., Harris D., Rajandream M., Ivens A., Barrell B.,
 RA Oliver K.;
 RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AL390114; CAB98658.2;
 DR InterPro: IPR001611; LRR.
 DR InterPro: IPR003592; LRR_out.
 DR Pfam: PF00560; LRR; 3.
 DR SMART: SM00370; LRR; 3.

SQ SEQUENCE 345 AA; 37530 MW; 06ECC850B1B54B70 CRC64;
 Query Match
 Best Local Similarity 7.9%; Score 98.5; DB 5; Length 345;
 Matches 56; Conservative 21; Mismatches 57; Indels 101; Gaps 10;
 QY 6 PAMSPPTYLLLLLLSSGSLG-----QDCSFQHSPISSDPAVKIRELS 49
 DB 152 PEMGWSLTSVNLNGTGTSGTLPPQWSGMSKARSLQDDCLSGSLPSSMSAI----- 205
 QY 50 DYLLQDYPTVAVASNLQDEELCG-----GLRLVLAQRMMERLKVAGSKMGLLEVRNTE 104
 DB 206 -----PMLASVSLAKNKEFCVCRTRGRRLVLL--WTSKISTRATA----- 245
 QY 105 IHFVTKAFQF---PPSCIRFVQNTISRLLOETSEQLVAKWITRONFSRCLLQCCPD 161
 DB 246 --WLLRTAQRPLSPPPQRPRTSLT-----FPLRRGR 278
 QY 162 SSTLPSPWSPRLLEATAPAPQPLLLL---LLPVGLLLLAAMCLHMQRTR 212
 DB 279 LSRLLQPALRRRLN-----PQPLRLRLNRPRLP-----QQTR 313
 RESULT 13
 Q9DMH8
 ID 09DMH8 PRELIMINARY; PRT: 1240 AA.
 AC 09DMH8;
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE Pcr.
 GN R2.
 OS Rat cytomegalovirus (strain Maastricht).
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Betaherpesvirinae; Muromegalovirus.
 OC NCBI_TaxID=79700;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MAASTRICHT;
 RX MEDLINE=20366325; PubMed=10906222;
 RA Vink C., Beuken E., Bruggeman C.A.;
 RT "Complete DNA sequence of the rat cytomegalovirus genome."
 RL J. Virol. 74:7656-7665(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MAASTRICHT;
 RX MEDLINE=20473137; PubMed=11018281;
 RA Grulithuisen Y.K., Beuken E., Bruggeman C.A., Vink C.;
 RT "Rat cytomegalovirus R89 is a highly conserved gene which expresses a
 RT spliced transcript."
 RL Virus Res. 69:119-130(2000).
 DR EMBL: AF32689; AAF99111.1;
 SQ SEQUENCE 1240 AA; 125612 MW; 33B6C13DC6A272B0 CRC64;
 Query Match
 Best Local Similarity 7.7%; Score 95.5; DB 12; Length 1240;
 Matches 29; Conservative 8; Mismatches 18; Indels 33; Gaps 5;
 QY 160 PDSSSTL-----PPWSRP--LEATAPAPQ--PLLLLLLPVGLLLAA 201
 DB 1060 PDSTAVTGATTERSPATEPRPRRLPPGVSAPLAQPITLLSLVPA----- 1112
 QY 202 AMCLHMQRTRRRTPRPGQVPPVPSPD 229
 DB 1113 -----QATRASPPRETDAF--PTPAD 1132
 RESULT 14
 Q9C5T0
 ID 09C5T0 PRELIMINARY; PRT: 658 AA.
 AC 09C5T0;
 DT 01-JUN-2001 (Tremblrel. 17, Created)
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)

DT 01-MAR-2002 (TREMBLrel. 20, last annotation update)
DE Receptor-like protein kinase 4.
GN Ruk4.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20575726; Pubmed=11135117;
RA Du L., Chen Z.;
RT "Identification of genes encoding receptor-like protein kinases as
RT possible targets of pathogen- and salicylic acid-induced WRKY DNA-
RT binding proteins in Arabidopsis";
RL Plant J. 24:837-847(2000).
DR EMBL: AF224705; AAK28315.1; -
DR InterPro: IPR002902; DUF26.
DR InterPro: IPR000719; Euk_Pkinase.
DR InterPro: IPR002290; Ser_thr_Pkinase.
DR InterPro: IPR001245; Tyr_Pkinase.
DR Pfam: PF01657; DUF26; 2.
DR Pfam: PF00069; Pkinase; 1.
DR ProDom: PD000001; Euk_Pkinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR SMART: SM00219; TYKc; 1.
DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE: PS50011; PROTEIN KINASE_DOM; 1.
DR ATP-binding; kinase; transferase.
SO SEQUENCE 658 AA; 72991 MW; DCF9CF5F1748F614 CRC64;

GenCore version 5.1.4.P5.4578
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OM protein - protein search, using sw model

Run on: May 27, 2003, 18:24:51 ; Search time 36 seconds
(without alignments)
869,830 Million cell updates/sec

Title: US-08-994-468-6
Perfect score: 1242
Sequence: 1 MVLAPAWSPFTYLLLLLL.....

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 908470 seqs, 133250620 residues
Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

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| 1: | /SID2/gcgdata/geneq/geneq-emb1/AA1980.DAT* |
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| 3: | /SID2/gcgdata/geneq/geneq-emb1/AA1982.DAT* |
| 4: | /SID2/gcgdata/geneq/geneq-emb1/AA1983.DAT* |
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| 6: | /SID2/gcgdata/geneq/geneq-emb1/AA1985.DAT* |
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| 13: | /SID2/gcgdata/geneq/geneq-emb1/AA1992.DAT* |
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| 20: | /SID2/gcgdata/geneq/geneq-emb1/AA1999.DAT* |
| 21: | /SID2/gcgdata/geneq/geneq-emb1/AA2000.DAT* |
| 22: | /SID2/gcgdata/geneq/geneq-emb1/AA2001.DAT* |
| 23: | /SID2/gcgdata/geneq/geneq-emb1/AA2002.DAT* |

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No | Score | Query Match | Length | DB ID | Description |
|-----------|-------|-------------|--------|-------|-------------|
| 1 | 1242 | 100.0 | 235 | 16 | AA67541 |
| 2 | 1242 | 100.0 | 235 | 20 | AA67769 |
| 3 | 1242 | 100.0 | 235 | 21 | AA69719 |
| 4 | 1242 | 100.0 | 235 | 22 | AA620192 |
| 5 | 1242 | 100.0 | 235 | 23 | AA608129 |
| 6 | 1236 | 99.5 | 235 | 16 | AA66175 |
| 7 | 1236 | 99.5 | 235 | 22 | AA620194 |
| 8 | 1124 | 90.5 | 212 | 21 | AA69721 |
| 9 | 1114 | 89.7 | 209 | 19 | AA69007 |
| 10 | 1114 | 89.7 | 209 | 21 | AA69720 |

| | | | | | | |
|----|-------|------|-----|----|----------|----------------------------|
| 11 | 1110 | 89.4 | 209 | 21 | AA69723 | Human flt-3 mutein |
| 12 | 1110 | 89.4 | 209 | 21 | AA69726 | Human flt-3 mutein |
| 13 | 1110 | 89.4 | 209 | 21 | AA69727 | Human flt-3 mutein |
| 14 | 1110 | 89.4 | 209 | 21 | AA69729 | Human flt-3 mutein |
| 15 | 1110 | 89.2 | 209 | 21 | AA69722 | Human flt-3 mutein |
| 16 | 1108 | 89.2 | 209 | 21 | AA69724 | Human flt-3 mutein |
| 17 | 1107 | 89.1 | 209 | 21 | AA69728 | Human flt-3 mutein |
| 18 | 1100 | 88.6 | 209 | 21 | AA69725 | Human flt-3 mutein |
| 19 | 970 | 78.1 | 185 | 22 | AA620195 | Human flt-3 ligand |
| 20 | 895.5 | 72.1 | 294 | 21 | AA58204 | Human flt-3 ligand |
| 21 | 894.5 | 72.0 | 291 | 21 | AA58210 | Feline flt-3 ligand |
| 22 | 834 | 67.1 | 178 | 22 | AA620193 | Human flt-3 ligand |
| 23 | 797.5 | 64.2 | 268 | 21 | AA58206 | Canine mature flt-3 ligand |
| 24 | 796.5 | 64.1 | 276 | 21 | AA58207 | Canine mature flt-3 ligand |
| 25 | 791.5 | 63.7 | 265 | 21 | AA58211 | Feline mature flt-3 ligand |
| 26 | 768.5 | 61.9 | 231 | 16 | AA67540 | Mouse flt-3 ligand |
| 27 | 768.5 | 61.9 | 231 | 20 | AA67768 | Mouse flt-3 ligand |
| 28 | 768.5 | 61.9 | 231 | 22 | AA620186 | Mouse flt-3 ligand |
| 29 | 768 | 61.8 | 232 | 16 | AA66177 | Mouse flt-3 ligand |
| 30 | 764 | 61.5 | 232 | 22 | AA620189 | Mouse flt-3 ligand |
| 31 | 745 | 60.0 | 150 | 19 | AA67930 | Human flt-3 ligand |
| 32 | 745 | 60.0 | 150 | 19 | AA69054 | Human flt-3 ligand |
| 33 | 740.5 | 59.6 | 377 | 19 | AA678124 | Human flt-3 ligand |
| 34 | 739 | 59.5 | 143 | 19 | AA67926 | Human flt-3 ligand |
| 35 | 739 | 59.5 | 143 | 19 | AA69050 | Human flt-3 ligand |
| 36 | 737.5 | 59.4 | 349 | 19 | AA683289 | Human flt-3 ligand |
| 37 | 737.5 | 59.4 | 349 | 19 | AA68005 | Human flt-3 ligand |
| 38 | 736.5 | 59.3 | 340 | 19 | AA683291 | Human flt-3 ligand |
| 39 | 736.5 | 59.3 | 349 | 19 | AA683286 | Human flt-3 ligand |
| 40 | 736.5 | 59.3 | 523 | 19 | AA68008 | Human flt-3 ligand |
| 41 | 735 | 59.2 | 140 | 19 | AA67911 | Human flt-3 ligand |
| 42 | 735 | 59.2 | 140 | 19 | AA69035 | Human flt-3 ligand |
| 43 | 735 | 59.2 | 144 | 19 | AA67928 | Human flt-3 ligand |
| 44 | 735 | 59.2 | 144 | 19 | AA69052 | Human flt-3 ligand |
| 45 | 735 | 59.2 | 313 | 19 | AA683294 | Human flt-3 ligand |

ALIGNMENTS

RESULT 1
ID AAR67541 standard; protein: 235 AA.

AC AAR67541;
DT 05-AUG-1995 (first entry)
XX

DE Human flt-3 ligand.

XX flt-3 ligand; flt3-L; anemia; cancer; AIDS; gene therapy.

XX Homo sapiens.

OS Homo sapiens.

PH Key

FT Peptide

FT Location/Qualifiers

FT 1..26

FT /note- "Signal peptide may extend to position 27"

FT 27..182

FT /label- "Extracellular domain

FT /note- "extracellular domain may start at position 28"

FT 183..205

FT /label- "Transmembrane domain

FT 206..235

FT /label- "Cytoplasmic domain

PN EP627487-A.

XX

PD 07-DEC-1994.

XX

PF 19-MAY-1994; 94EP-0303575.

XX

24-MAY-1993; 93US-0068394.
 PR 12-AUG-1993; 93US-0106463.
 PR 25-AUG-1993; 93US-0111758.
 PR 03-DEC-1993; 93US-0162407.
 PR 07-MAR-1994; 94US-0209502.
 PR 11-MAY-1994; 94US-0243545.
 XX
 PA (IMMUNEX) IMMUNEX CORP.
 XX
 PI Beckmann MP, Lyman SD;
 XX
 DR WPI: 1995-008071/02.
 DR N-PSDB: AA079079.
 XX
 PT Isolated ligands for flt3 receptors - useful for treating
 XX anemias, AIDS and various cancers
 XX
 PS Disclosure: Page 29-30; 33pp; English.
 XX
 CC A human T-cell lambda-gli0 random primed cDNA library was
 CC screened with a fragment corresponding to the extracellular
 CC domain of mouse flt3 ligand (flt3-L) (nt 103-516 of AA079076)
 CC to isolate human flt3-L cDNA. Flt-3 stimulates progenitor and
 CC stem cells, and can be used e.g. in gene therapy protocols.
 CC
 XX
 SQ Sequence 235 AA;
 XX
 Query Match 100.0%; Score 1242; DB 16; Length 235;
 Best Local Similarity 100.0%; Pred. No. 5e-109;
 Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTVLPAWSPPTTYLLLLSSGLSTGDCSFQHSFISDFAKIRELSDYLDQDPVTV 60
 DB 1 MTVLPAWSPPTTYLLLLSSGLSTGDCSFQHSFISDFAKIRELSDYLDQDPVTV 60
 QY 61 ASNLODEELCGGLMRLVLAQRMERLKTAVAGSKMGLLEVRNTEIHFTVKCAEQPPSCL 120
 DB 61 ASNLODEELCGGLMRLVLAQRMERLKTAVAGSKMGLLEVRNTEIHFTVKCAEQPPSCL 120
 QY 121 REVQTNISRLQETSEQLVALKPWITRONFSRCLQLCCPDSTLPPWSPRELEATAPT 180
 DB 121 REVQTNISRLQETSEQLVALKPWITRONFSRCLQLCCPDSTLPPWSPRELEATAPT 180
 QY 181 APOPELLLLLPVGLLLAAWCLHMORTRRPRPGEQVPPVSPDQLLVEH 235
 DB 181 APOPELLLLLPVGLLLAAWCLHMORTRRPRPGEQVPPVSPDQLLVEH 235
 RESULT 2
 AA67769
 ID AA67769 standard; Protein: 235 AA.
 AC AA67769;
 DT 25-MAR-1999 (first entry)
 XX
 DE Human flt3-ligand.
 XX
 KW Antigen-specific peripheral immune tolerance; flt3-ligand; flt3-L;
 KW immunogenic; autoimmune disease; organ transplantation; food allergy;
 KW tissue transplantation.
 XX
 OS Homo sapiens.
 XX
 PN W09857655-A1.
 XX
 PD 23-DEC-1998.
 XX
 PF 12-JUN-1998; 98MO-US12085.
 XX
 PR 17-JUN-1997; 97US-0877421.
 XX
 PA (IMMUNEX) IMMUNEX CORP.

XX
 PI Abbott NM, Mowat AM, Viney JL;
 XX
 DR WPI: 1999-070422/06.
 DR N-PSDB: AAV81506.
 XX
 PT Methods for initiating or enhancing antigen specific immune
 PT tolerance - by using murine or human flt3 ligand
 XX
 PS Claim 1: Page 14-15; 25pp; English.
 XX
 CC A method has been developed of initiating or enhancing: (i) an antigen-
 CC specific immune tolerance; or (ii) immunotolerance of a therapeutic
 CC immunogenic molecule by addition of a polypeptide, before, after or with
 CC the mucosal administration of an immunotolerising amount of the antigen
 CC or therapeutic molecule, respectively. The polypeptide is capable of
 CC binding the flt3 receptor and is: a) amino acids 28-x of murine flt3
 CC ligand (flt3-L), where x is an amino acid between 163-231; b) amino
 CC acids 28-y of human flt3-L, where y is an amino acid between 160-235;
 CC and c) a polypeptide that has at least 90% identity to the polypeptides
 CC of either (a) or (b). The method ameliorates the effects of autoimmune
 CC diseases, food allergies or organ or tissue rejection following
 CC transplantation. Administration of flt3-L allows lower doses of antigens
 CC to be used in vivo for mucosally administered antigens. The present
 CC sequence represents human flt3-L.
 CC
 XX
 SQ Sequence 235 AA;
 XX
 Query Match 100.0%; Score 1242; DB 20; Length 235;
 Best Local Similarity 100.0%; Pred. No. 5e-109;
 Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTVLPAWSPPTTYLLLLSSGLSTGDCSFQHSFISDFAKIRELSDYLDQDPVTV 60
 DB 1 MTVLPAWSPPTTYLLLLSSGLSTGDCSFQHSFISDFAKIRELSDYLDQDPVTV 60
 QY 61 ASNLODEELCGGLMRLVLAQRMERLKTAVAGSKMGLLEVRNTEIHFTVKCAEQPPSCL 120
 DB 61 ASNLODEELCGGLMRLVLAQRMERLKTAVAGSKMGLLEVRNTEIHFTVKCAEQPPSCL 120
 QY 121 REVQTNISRLQETSEQLVALKPWITRONFSRCLQLCCPDSTLPPWSPRELEATAPT 180
 DB 121 REVQTNISRLQETSEQLVALKPWITRONFSRCLQLCCPDSTLPPWSPRELEATAPT 180
 QY 181 APOPELLLLLPVGLLLAAWCLHMORTRRPRPGEQVPPVSPDQLLVEH 235
 DB 181 APOPELLLLLPVGLLLAAWCLHMORTRRPRPGEQVPPVSPDQLLVEH 235
 RESULT 3
 AAV69719
 ID AAV69719 standard; Protein: 235 AA.
 AC AAV69719;
 DT 05-JUL-2000 (first entry)
 XX
 DE Full length wild type human flt-3 protein.
 XX
 KW Immunomodulator; immunosuppressive; cytostatic; antianemic; anti-HIV;
 KW neuroprotective; anti-allergic; flt3 ligand; flt3-L; wild type; allergy;
 KW cell surface tyrosine kinase receptor; hematopoietic progenitor cell;
 KW cellular expansion; cellular differentiation; natural killer cell;
 KW cancer; dendritic cell; immune response; autoimmunity; immunosuppression;
 KW myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;
 KW multiple myeloma; leukemia.
 XX
 OS Homo sapiens.
 XX
 PN W0200001823-A2.
 XX
 PD 13-JAN-2000.

PF 25-JUN-1999; 99WO-US14296.
 XX 02-JUL-1998; 98US-0109100.
 XX (IMMUNEX CORP.
 PA Graddis TJ, McGrew JT;
 XX WPI, 2000-182115/16.
 DR N-PSDB; AAF59064.
 XX
 PT Mutant soluble flt3 ligand polypeptide used in cellular expansion,
 PT immune response stimulation or treatment of pathological conditions
 PT contains amino acid substitutions at positions 8, 84, 118 or 122
 XX
 PS Claim 1: Page 72-73; 90pp; English.

CC The invention relates to novel soluble flt3 ligand (flt3-l) polypeptides
 CC which exhibits increased or decreased biological activity relative to
 CC the full length wild type (this sequence) or mature (AA60720) flt3-l
 CC polypeptides. The flt3-l protein binds cell surface tyrosine kinase
 CC receptors and regulate growth and differentiation of hematopoietic
 CC progenitor cells. The flt3-l protein can be used to induce cellular
 CC hematopoietic, natural killer (NK) or dendritic cells, especially in the
 CC presence of growth factors such as interleukins, colony stimulating
 CC factors or protein kinases. The protein can also modulate, augment or
 CC enhance a patient's immune response and can be used to treat an immune
 CC disorder (e.g. allergy, autoimmunity or immunosuppression). The protein
 CC may be used to treat a pathological condition e.g. myelodysplasia,
 CC aplastic anemia, HIV infection, breast, small cell lung, testicular or
 CC ovarian cancer, lymphoma, multiple myeloma, neuroblastoma or acute
 CC leukemia.
 XX
 SO Sequence 235 AA:

Query Match 100.0%; Score 1242; DB 21; Length 235;
 Best Local Similarity 100.0%; Pred. No. 5e-109;
 Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MTVALPAMSPPTTYLLLLLSGSGTODCSFQHSPISSDFAVKIRELSYLLQDVPVY 60
 DB 1 MTVALPAMSPPTTYLLLLLSGSGTODCSFQHSPISSDFAVKIRELSYLLQDVPVY 60
 OY 61 ASNLODEELCGGLMRLVLAQRMRERLKTVAAGSKMGLLRVMTIEHFVTKCAFOPPSCL 120
 DB 61 ASNLODEELCGGLMRLVLAQRMRERLKTVAAGSKMGLLRVMTIEHFVTKCAFOPPSCL 120
 OY 121 RFVQTNISRLQETSEQLVALKPWITRONFSRCLQCPDSSSTLPPMSPRLATAPT 180
 DB 121 RFVQTNISRLQETSEQLVALKPWITRONFSRCLQCPDSSSTLPPMSPRLATAPT 180
 OY 181 APQPPPLLLLPVGLLLAAAMCLHMORTRRRTPRGQVPPVPODLLVEH 235
 DB 181 APQPPPLLLLPVGLLLAAAMCLHMORTRRRTPRGQVPPVPODLLVEH 235

RESULT 4
 AAB20192
 ID AAB20192 standard; Protein: 235 AA.

AC AAB20192;
 XX
 DT 14-MAY-2001 (first entry)
 XX
 DE Human Flt-3 ligand.
 XX
 KM Flt-3 ligand; Fms-like tyrosine kinase; human; vaccine;
 KM immunotherapy; therapy; tumour; cancer; melanoma; glioma;
 KM lymphoma; autoimmune disease; infection; gene therapy.
 OS Homo sapiens.
 XX

FH Key Location/Qualifiers
 FT Peptide 1..26
 FT Protein /label- signal_peptide
 FT Protein 27..235
 FT Domain /label- Mature-protein
 FT Domain 27..182
 FT Domain /label- Extracellular_domain
 FT Domain 183..205
 FT Domain /label- Transmembrane_domain
 FT Domain 206..235
 FT Domain /label- Cytoplasmic_domain
 PN W0200109303-A2.
 XX
 PD 08-FEB-2001.
 XX
 PF 31-JUL-2000; 2000WO-US20679.
 XX
 PR 30-JUL-1999; 99US-0146170.
 XX
 PA (VICA-) VICAL INC.
 XX
 PI Hermanson GG;
 DR WPI, 2001-123319/13.
 DR N-PSDB; AAF30310.
 XX
 PT Immunogenic compositions comprising flt-3 ligand encoding
 PT polynucleotide and one or more antigen, or cytokine encoding
 PT polynucleotides, useful for suppressing tumour growth and for treating
 PT autoimmune diseases (e.g. rheumatoid arthritis) -
 XX
 PS Claim 2: Page 132-133; 149pp; English.

CC The present sequence is that of human Fms-like tyrosine kinase
 CC (Flt-3 ligand). The invention is directed to enhancing the
 CC immune response of a vertebrate to an antigen or a cytokine by
 CC administering in vivo, into a tissue of a vertebrate, a Flt-3
 CC ligand-encoding polynucleotide, and 1 or more antigen- or
 CC cytokine-encoding polynucleotides. The flt-3 ligand-encoding
 CC polynucleotide may encode the present full-length human flt-3
 CC ligand polypeptide, or amino acids 27-160, 1-160, 27-185, 1-185,
 CC or 27-235 of the ligand. The polynucleotides are incorporated
 CC into the cells of the vertebrate in vivo, and a prophylactically
 CC or therapeutically effective amount of flt-3 ligand and 1 or more
 CC antigens or cytokines is produced in vivo. Pharmaceutical
 CC compositions comprising the polynucleotides are useful for
 CC suppressing tumour growth in a mammal. The tumour is melanoma,
 CC glioma or lymphoma, particularly B-cell lymphoma. They can also
 CC be used for the prophylactic and/or therapeutic treatment of:
 CC (a) bacterial (e.g. Bacillus infections), viral (e.g. hepatitis B
 CC and C in humans), parasitic (e.g. malaria) and fungal infections;
 CC (b) autoimmune diseases (e.g. rheumatoid arthritis and
 CC osteoarthritis); (c) cancer; and (d) Aujeszky's disease in pigs.
 CC Various other examples of these diseases are given in the
 CC specification.
 XX

SO Sequence 235 AA:
 Query Match 100.0%; Score 1242; DB 22; Length 235;
 Best Local Similarity 100.0%; Pred. No. 5e-109;
 Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MTVALPAMSPPTTYLLLLLSGSGTODCSFQHSPISSDFAVKIRELSYLLQDVPVY 60
 DB 1 MTVALPAMSPPTTYLLLLLSGSGTODCSFQHSPISSDFAVKIRELSYLLQDVPVY 60
 OY 61 ASNLODEELCGGLMRLVLAQRMRERLKTVAAGSKMGLLRVMTIEHFVTKCAFOPPSCL 120
 DB 61 ASNLODEELCGGLMRLVLAQRMRERLKTVAAGSKMGLLRVMTIEHFVTKCAFOPPSCL 120
 OY 121 RFVQTNISRLQETSEQLVALKPWITRONFSRCLQCPDSSSTLPPMSPRLATAPT 180
 DB 121 RFVQTNISRLQETSEQLVALKPWITRONFSRCLQCPDSSSTLPPMSPRLATAPT 180

DB 121 REVQTNISRLQETSDQVLAALKPMWITRONFSRCLQCOQDSSSTLPSPMSRPLEATAPT 180
 QY 181 AQPPLLLLLLPLVGLLLAAAMCLHWQTRRRTPRPGQVPPVPSQDILLVEH 235
 DB 181 AQPPLLLLLLPLVGLLLAAAMCLHWQTRRRTPRPGQVPPVPSQDILLVEH 235

RESULT 5
 ABB08129 standard; protein; 235 AA.
 ID ABB08129
 XX ABB08129;
 AC ABB08129;
 XX 10-SEP-2002 (first entry)
 DT 10-SEP-2002 (first entry)
 XX Human Flt3L polypeptide.
 DE Human Flt3L polypeptide.
 XX Dendritic cell; mobilisation factor; T cell; adjuvant; antibacterial;
 KW fungicide; protozoacide; virucide; anti-inflammatory; anti-HIV;
 KW tuberculostatic; cytostatic; human; Flt3L.
 XX Homo sapiens.
 OS Homo sapiens.
 XX WO20036141-A2.
 PN 10-MAY-2002.
 PD 10-MAY-2002.
 XX 30-OCT-2001; 2001WO-0544834.
 PF 02-NOV-2000; 2000US-245721P.
 PR 02-NOV-2000; 2000US-245721P.
 PA (IMM) IMMUNEX CORP.
 XX Lynch DH, De Smedt TN, Maliszewski CR, Butz EA, Miller RE
 PI Thomas EK;
 DR WPI; 2002-500114/53.
 XX
 PT Treating an individual suffering from infection, e.g. inflammation,
 PT chickenpox or AIDS, by administering a combination of dendritic cell
 PT mobilization factor or maturation agent, T cell enhancing factor and
 PT antigen-specific T cells -
 PT
 XX
 PS Disclosure; Page 37-38; 43pp; English.
 XX
 CC The invention relates to treating an individual at risk for or suffering
 CC from infection with a pathogenic or opportunistic organism. The method
 CC involves administering a combination of two to five agents comprising:
 CC (a) dendritic cell mobilisation factor; (b) dendritic cell maturation
 CC agent; (c) dendritic cell activation agent; (d) T cell enhancing factor;
 CC or (e) activated, antigen-specific T cells. The methods are useful for
 CC treating an individual at risk for or suffering from infection with a
 CC pathogenic or opportunistic organism, e.g. viruses (e.g. HIV), bacteria
 CC (e.g. M. tuberculosis), yeast, fungi (e.g. C. albicans) or protozoa (e.g.
 CC T. cruzi, which causes Chagas disease). The methods are especially
 CC useful for treating an individual suffering from immunosuppression by
 CC enhancing a lymphocyte-mediated immune response. In particular, the
 CC method is useful for treating inflammation, chickenpox, oral or genital
 CC herpes, mononucleosis, multifocal leukoencephalopathy, hepatitis, AIDS,
 CC T cell leukemia or T cell lymphoma. The activated antigen-presenting
 CC dendritic cells are useful as a vaccine adjuvant. The present sequence
 CC represents a human Flt3L polypeptide fragment, that can be used as a
 CC dendritic cell mobilisation factor.
 CC
 XX
 SO Sequence 235 AA:

Query Match 100.0%; Score 1242; DB 23; Length 235;
 Best Local Similarity 100.0%; Pred. No. 5e-109;
 Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYTAAAPMSPTTLLLLLSGLSGTDCSFGHSPISDFAVKIRLSDYLQDVPVTV 60
 DB 1 MYTAAAPMSPTTLLLLLSGLSGTDCSFGHSPISDFAVKIRLSDYLQDVPVTV 60

QY 61 ASNLODEELCGGLMRVLAQRMWERLKVAGSKMGLLEBVENEIHFTKCAQPPSPSCL 120
 DB 61 ASNLODEELCGGLMRVLAQRMWERLKVAGSKMGLLEBVENEIHFTKCAQPPSPSCL 120
 QY 121 REVQTNISRLQETSDQVLAALKPMWITRONFSRCLQCOQDSSSTLPSPMSRPLEATAPT 180
 DB 121 REVQTNISRLQETSDQVLAALKPMWITRONFSRCLQCOQDSSSTLPSPMSRPLEATAPT 180
 QY 181 AQPPLLLLLLPLVGLLLAAAMCLHWQTRRRTPRPGQVPPVPSQDILLVEH 235
 DB 181 AQPPLLLLLLPLVGLLLAAAMCLHWQTRRRTPRPGQVPPVPSQDILLVEH 235

RESULT 6
 AAR66175 standard; Peptide; 235 AA.
 ID AAR66175
 XX AAR66175;
 AC AAR66175;
 XX 10-AUG-1995 (first entry)
 DT 10-AUG-1995 (first entry)
 XX Human S86/S109 Flt3 ligand peptide sequence.
 DE Human S86/S109 Flt3 ligand peptide sequence.
 XX Flt3 ligand; tyrosine kinase receptor ligand.
 KW Homo sapiens.
 OS Homo sapiens.
 XX WO9426891-A.
 PN 24-NOV-1994.
 PD 24-NOV-1994.
 XX 18-MAY-1994; 94MO-US05150.
 PF 19-MAY-1993; 93US-0065231.
 PR 07-JUL-1993; 93US-0068263.
 PR 16-JUL-1993; 93US-0092549.
 PR 13-AUG-1993; 93US-0106340.
 PR 24-AUG-1993; 93US-0112391.
 PR 19-NOV-1993; 93US-0155111.
 PR 03-DEC-1993; 93US-0162413.
 XX
 PA (INRM) INST NAT SANTE & RECH MEDICALE.
 PA (SCHE) SCHERING CORP.
 XX
 PI Birnbaum D, Culpepper JA, Hannum CH, Lee FD;
 DR WPI; 1995-006787/01.
 XX N-PSDB; AA079642.
 XX
 PT New ligand for the Flt3 tyrosine kinase receptor - and related
 PT nucleic acid, vectors, host cells and antibodies, useful for
 PT treating abnormal cell physiology and proliferation, e.g. cancer,
 PT also for diagnosis and drug screening
 PT
 XX
 PS Claim 11; Page 76-77; 90pp; English.
 XX
 CC A cDNA library from the human stromal cell line 293v48, in
 CC pME185, was screened with an 800 bp fragment derived from
 CC mouse clone T110. This fragment encompasses the coding region
 CC conserved between two mouse clones, T118 and T110. Approx. 20
 CC positive clones were selected and partially sequenced. Two
 CC clones, S86 and S109, were found to be approx. 75% homologous
 CC to the mouse clones over the first 163 AAs. Clone S86 continued
 CC to show homology to T110 until the stop codon, although to a
 CC lesser degree, for an overall homology of 66%. Clones T118 and
 CC S109 do not show homology to each other or to the other clones
 CC after mouse residue 163 (human residue 160). An additional mouse
 CC clone designated M88 has a 29 AA insert at the junction between
 CC the common and divergent portions of the mouse ligand.
 CC
 XX
 SO Sequence 235 AA:

| | Query Match | 99.5% | Score 1236; | DB 16 | Length 235; |
|----|-----------------------|---|--------------------|--------------|---------------|
| | Best Local Similarity | 99.6% | Prod. No. 1.8e-108 | | |
| | Matches 234; | Conservative | 0; | Mismatches 1 | Indels 0 Gaps |
| QY | 1 | MTVLPAWSPPTYYLLLLLSGLSGTODCSFHSHPISDFAVKIREISDVLQDYPITY | 60 | | |
| Db | 1 | MTVLPAWSPPTYYLLLLLSGLSGTODCSFHSHPISDFAVKIREISDVLQDYPITY | 60 | | |
| QY | 61 | ASNODELCSGLKMLVLAQRMMEKLKVAGSKMOGLLEVRNTEIHEVTKCAFQPPSCL | 120 | | |
| Db | 61 | ASNODEELCSGLKMLVLAQRMMEKLKVAGSKMOGLLEVRNTEIHEVTKCAFQPPSCL | 120 | | |
| QY | 121 | RFVQTNISRLLOETSQVLAKPMYTRNCFSCLELCQOPSSSTLPMPMSRPLEATPPT | 180 | | |
| Db | 121 | RFVQTNISRLLOETSQVLAKPMYTRNCFSCLELCQOPSSSTLPMPMSRPLEATPPT | 180 | | |
| QY | 181 | APQPPLLLLLLLPVGLLLLAAMCLHMORTRRRRPRPCEQVPVPVPSPODLLLVH | 235 | | |
| Db | 181 | APQPPLLLLLLLPVGLLLLAAMCLHMORTRRRRPRPCEQVPVPVPSPODLLLVH | 235 | | |

| | |
|----|--|
| | RESULT 7 |
| ID | AAB20194 |
| XX | AAB20194 standard; Protein; 235 AA. |
| AC | |
| XX | AAB20194; |
| DF | 14-MAY-2001 (first entry) |
| XX | |
| DE | Human Flt-3 ligand. |
| KW | Flt-3 ligand; Fms-like tyrosine kinase; human; vaccine; immunotherapy; therapy; tumour; cancer; melanoma; glioma; lymphoma; autoimmune disease; infection; gene therapy. |
| XK | |
| OS | Homo sapiens. |
| XX | |
| FT | Key Location/Qualifiers |
| FT | Peptide 1..26 |
| FT | /label= Signal_peptide 27..235 |
| FT | /label= Mature_protein 27..182 |
| FT | Domain /label= Extracellular_domain 183..205 |
| FT | Domain /label= Transmembrane_domain 206..235 |
| FT | Domain /label= Cytoplasmic_domain |
| PX | |
| PN | WO200109303-A2. |
| PD | |
| XX | 08-FEB-2001. |
| PF | 31-JUL-2000; 200OWO-US20679. |
| PR | 30-JUL-1999; 99US-0146170. |
| PA | (VICA-) VICAL INC. |
| PI | Hermanson GG; |
| DR | WP1: 2001-123319/13. N-PSDB: AAF30312. |
| PT | Immunogenic compositions comprising Flt-3 ligand encoding polynucleotide and one or more antigen, or cytokine encoding polynucleotides, useful for suppressing tumour growth and for treating autoimmune diseases (e.g. Rheumatoid arthritis). |
| CC | Claim 2; Page 137-138; 14pp; English. The present sequence is that of human Fms-like tyrosine kinase (Flt-3 ligand). The invention is directed to enhancing the |

immune response of a vertebrate to an antigen or a cytokine by administering *in vivo*, into a tissue of a vertebrate, a Flt-3 ligand-encoding polynucleotide, and 1 or more antigen- or cytokine-encoding polynucleotides. The Flt-3 ligand-encoding polynucleotide may encode the present full-length human Flt-3 ligand polypeptide, or amino acids 27-185, 1-185, 27-235 or 1-235 of the Flt-3 ligand. The polynucleotides are incorporated into the cells of the vertebrate *in vivo*, and a prophylactically or therapeutically effective amount of Flt-3 ligand and 1 or more antigens or cytokines is produced *in vivo*. Pharmaceutical compositions comprising the polynucleotides are useful for suppressing tumour growth in a mammal. The tumour is melanoma, glioma or lymphoma, particularly B-cell lymphoma. They can also be used for the prophylactic and/or therapeutic treatment of: (a) bacterial (e.g. *Bacillus* infections), viral (e.g. hepatitis B and C in humans), parasitic (e.g. malaria) and fungal infections; (b) autoimmune diseases (e.g. rheumatoid arthritis and osteoarthritis); (c) cancer; and (d) Aujeszky's disease in pigs. Various other examples of these diseases are given in the specification.

| Query Match | Best Local Similarity | Score 1236; | DB 22; | Length 235; |
|--------------|---|-------------|-----------------|-------------|
| Matches 234; | Conservative | 0; | Mismatches 108; | Indels 0; |
| Gaps | | | | |
| Qy 1 | MVLPAWSPPTYYLLLLLLSSGSLGTQDCSPHSPISDFPAVKIRLSDYLDDYPPVY | 60 | | |
| Db 1 | MVLPAWSPPTYYLLLLLLSSGSLGTQDCSPHSPISDFPAVKIRLSDYLDDYPPVY | 60 | | |
| Qy 61 | ASNLDDEELCGGLMRLVLAQRMNERLKTVAAGSKMGGILLERVNTEIHFKCAFPSPSCL | 120 | | |
| Db 61 | ASNLDDEELCGGLMRLVLAQRMNERLKTVAAGSKMGGILLERVNTEIHFKCAFPSPSCL | 120 | | |
| Qy 121 | RVQVNTNISRLQETSEQVALKPMITRQNSFCLLQCCPDSSSTLPRLPPSPRLPNTAPT | 180 | | |
| Db 121 | RVQVNTNISRLQETSEQVALKPMITRQNSFCLLQCCPDSSSTLPRLPPSPRLPNTAPT | 180 | | |
| Qy 181 | APQPLLPLLLPLPVGLLLAAAMCLHMORTRRRTPRGQVPPVSPQDLLVHN | 235 | | |
| Db 181 | APQPLLPLLLPLPVGLLLAAAMCLHMORTRRRTPRGQVPPVSPQDLLVHN | 235 | | |
| RESULT 8 | | | | |
| ID | AA69721 | | | |
| AA69721 | standard; Protein; 212 AA. | | | |
| AC | AA69721; | | | |
| DT | 05-JUL-2000 (first entry) | | | |
| DE | Human flt-3 mutetin L-3H. | | | |
| KW | Immunomodulator; immunosuppressive; cytosstatic; antineumic; anti-HIV; | | | |
| KM | neuroprotective; antiallergic; flt3 ligand; flt3-L; wild type; allergy; | | | |
| KW | cell surface tyrosine kinase receptor; hematopoietic progenitor cell; | | | |
| KM | cellular expansion; cellular differentiation; natural killer cell; | | | |
| KW | cancer; dendritic cell; immune response; autoimmunity; immunosuppression; | | | |
| KM | myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma; | | | |
| KW | multiple myeloma; leukemia; mutetin. | | | |
| OS | Homo sapiens. | | | |
| OS | Synthetic. | | | |
| PN | MO200001823-A2. | | | |
| PD | 13-JAN-2000. | | | |
| PE | 25-JUN-1999; 99WO-US14296. | | | |
| PR | 02-JUL-1998; 98US-0109100. | | | |

PA (IMMUNEX CORP.
 XX
 PI Graddis TJ, McGrew JT;
 XX
 DR WPI, 2000-182115/16.
 XX
 PT Mutant soluble fliC ligand polypeptide used in cellular expansion,
 PT immune response stimulation or treatment of pathological conditions,
 PT contains amino acid substitutions at positions 8, 84, 118 or 122
 XX
 PS Claim 4; Page 79-80; 90pp; English.

The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides which exhibits increased or decreased biological activity relative to the full length wild type (AA69719) or mature (AA69720), flt3-L polypeptides. This sequence represents an example of the novel flt-3 ligands and comprises the L-3H mutant polypeptide. The flt3-L protein binds cell surface tyrosine kinase receptors and regulate growth and differentiation of hematopoietic progenitor cells. The flt3-L protein can be used to induce cellular expansion (especially in vivo) or differentiation, e.g. in hematopoietic, natural killer (NK) or dendritic cells, especially in the presence of growth factors such as interleukins, colony stimulating factors or protein kinases. The protein can also modulate, augment or enhance a patient's immune response and can be used to treat an immune disorder (e.g. allergy, autoimmunity or immunosuppression). The protein may be used to treat a pathological condition e.g. myelodysplasia, aplastic anemia, HIV infection, breast, small cell lung, testicular or ovarian cancer, lymphoma, multiple myeloma, neuroblastoma or acute leukemia.

SQ **Sequence** **212 AA;**

| | | | | |
|---------------------------|--------|-------------------|-------|-------------|
| Query Match | 90.5% | Score 1134 | DB 21 | Length 2125 |
| Best Local Similarity | 100.0% | Pred. NO. 5.9e-98 | | |
| Matches 211; Conservative | 0 | Mismatches | 0 | Gaps 0 |

| | | | |
|----|-----|---|-----|
| OY | 25 | STOQCSQPHSHISSISDFVKKRRELSYDLYOQPYTVANSLNDBEELCGIMRLVYAOXME | 84 |
| Db | 2 | STQDQCSQPHSHISSISDFVKKRRELSYDLYOQPYTVANSLNDBEELCGIMRLVYAOXME | 61 |
| OY | 85 | RLKTVAGSKMOGLLEVRNTEIHFTYKCAFOPBPSCLEFVQYNTISRLLOETSEOLVALKPM | 144 |
| Db | 62 | RLKTVAGSKMOGLLEVRNTEIHFTYKCAFOPBPSCRLVQYNTISRLLOETSEOLVALKPM | 122 |
| OY | 145 | ITRONFSKCLEOCQPBDSSTPPPMWSRPLBTKPAPQPLLLLLLPGLLELLAAAC | 204 |
| Db | 122 | ITRONFSKCLEOCQPBDSSTPPPMWSRPLBTKPAPQPLLLLLLPGLLELLAAAC | 181 |
| OY | 205 | LHMQRTRRRTRPGEQVPPVPSODLLLVH | 235 |
| Db | 182 | LHMQRTRRRTRPGEQVPPVPSODLLLVH | 212 |

RESULT 9

| ID | AAW69007 | standard; peptide; 209 AA |
|-----|----------|---------------------------|
| ... | | |

AC AAW69007

DT 01-OCT-1998 (first entry)

DE Human flt-3 receptor agonist.

KM Human; flt-3 receptor agonist; haematopoietic cell stimulation; cancer
 KW bone marrow reconstitution; hematological disease; immune deficiency;
 KW drug-induced myelosuppression; renal dialysis; gene therapy; infection;
 KM congenital metabolic disease; neurological disease; therapy;
 KW dendritic cell production.

OS Homo sapiens.

PN W09018923-A1

XX

PD 07-MAY-1998
YY

PF 23-OCT-1997; 97WO-US18700.

PR 25-OCT-1996; 96US-0030094.

PA (SEAR) SEARLE & CO G D.

PI Feng Y, McKearn JP, McWhorter CA, Minnerly JC, Munster NI;

XX

XX

p1 Rearranged *ilt-3* receptor agonists and nucleic acids encoding them
 p2 used to stimulate production of haematopoietic and dendritic cells,
 p3 for treatment of haematological diseases, bone marrow reconstitution
 p4 and in gene therapy

PS Disclosure; Page 9-10; 158pp; English.

CC This sequence represents a rearranged human flt-3 receptor agonists of
CC the invention. The agonists have a modified flt-3 ligand amino acid
CC sequence. The agonists are used to stimulate production of haematopoietic
CC cells *in vivo* (e.g. in a subject about to donate blood) or for *ex vivo*
CC expansion for subsequent transplantation, e.g. to reconstitute bone
CC marrow after chemotherapy, disease etc., or to treat haematological
CC disease such as drug-induced myelosuppression, defects caused by
CC infections, burns or renal dialysis. Optionally *ex vivo* expanded cells
CC are transduced with a gene therapy vector for treating e.g. congenital
CC metabolic diseases, immune deficiency, neurological disease, cancer and
CC infections. The agonists can also be used in the treatment of tumours,
CC infections and autoimmune disease, when administered optionally with an
CC antigen. The agonist can also be used in the production of dendritic
CC cells for use as an immunising adjuvant for treatment disorders including
CC acquired immune deficiency syndrome. Compared with native ligands, the
CC new agonists have better stimulatory activity, reduced side effects
CC and/or better physical properties such as solubility, stability or refold
CC efficiency. When used together with other stimulatory agents, the
CC agonists provide a synergistic effect.

SQ Sequence 209 AA:

| | | | | | | | |
|-----------------------|--------|--------------|---------|------------|----|--------|-----|
| Query Match | 89.7% | Score | 1114 | DB | 19 | Length | 209 |
| Best Local Similarity | 100.0% | Pred. No. | 5.1e-97 | | | | |
| Matches | 209 | Conservative | 0 | Mismatches | 0 | Indels | 0 |
| | | | | | | Gaps | 0 |

| | | | |
|----|-----|--|-----|
| Qy | 27 | TODCSFQSPJSSIPFAVKIRELSLYLLDQDYVTVYASNNODELCCGGIMRLVLAQRMERL | 8 |
| Dd | 1 | TODCSFQSPJSSIPFAVKIRELSLYLLDQDYVTVYASNNODELCCGGIMRLVLAQRMERL | 60 |
| Qy | 87 | KTVAGSKMOGLLERNYEIHFTVYKCAFOPPSCILREVOTNISRLLOETSEDLVAKFWIT | 146 |
| Dd | 61 | KTVAGSKMOGLLERNYEIHFTVYKCAFOPPSCILREVOTNISRLLOETSEDLVAKFWIT | 120 |
| Qy | 147 | RQNSRSCLELOCOPDSSILPPPPSPRPLEAATPAPOPLLLLLLRYGLLLLAAACLH | 200 |
| Dd | 121 | RQNSRSCLELOCOPDSSILPPPPSPRPLEAATPAPOPLLLLLLRYGLLLLAAACLH | 180 |
| Qy | 207 | WQTRRRTRPRGEGQVPPVPSPODLLLVH | 235 |
| Dd | 181 | WQTRRRTRPRGEGQVPPVPSPODLLLVH | 209 |

RESULT 10

ID AAY69720 standard; Protein; 209 AA.

AC AAY69720;

DT 05-JUL-2000 (first entry)

DE Mature wild type human flt-3 protein.

XX

| | | |
|----|---|---|
| ID | AA69723 | standard; Protein; 209 AA. |
| XX | | |
| AC | AA69723; | |
| XX | | |
| XX | | |
| DT | 05-JUL-2000 | (first entry) |
| XX | | |
| DE | Human flt-3 mutein K84E. | |
| XX | | |
| KW | Immunomodulator; immunosuppressive; cytostatic; antianemic; anti-HIV; | |
| KW | neuroprotective; anti-allergic; flt3 ligand; flt3-L; wild type; allergy; | |
| KW | cell surface tyrosine kinase receptor; hematopoietic progenitor cell; | |
| KW | cellular expansion; cellular differentiation; natural killer cell; | |
| KW | cancer; dendritic cell; immune response; autoimmunity; immunosuppression; | |
| KW | myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma; | |
| KW | multiple myeloma; leukemia; mutein. | |
| XX | | |
| OS | Homo sapiens. | |
| XX | Synthetic. | |
| PN | WO200001823-A2. | |
| XX | | |
| PD | 13-JAN-2000. | |
| XX | | |
| PF | 25-JUN-1999; 99WO-US14296. | |
| XX | | |
| PR | 02-JUL-1998; 98US-0109100. | |
| XX | | |
| PA | (IMMUNEX CORP. | |
| PI | Graddis TJ, McGrew JT; | |
| XX | | |
| DR | WPI; 2000-182115/16. | |
| XX | | |
| PT | Mutant soluble flt3 ligand polypeptide used in cellular expansion, | |
| XX | immune response stimulation or treatment of pathological conditions | |
| XX | contains amino acid substitutions at positions 8, 84, 118 or 122 | |
| XX | | |
| XX | Claim 4; Page 84-85; 90pp; English. | |
| XX | | |
| CC | The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides | |
| CC | which exhibits increased or decreased biological activity relative to | |
| CC | the full length wild type (AA69719) or mature (AA69720) flt3-L | |
| CC | polypeptides. This sequence represents an example of the novel flt3-L | |
| CC | ligands and comprises the K84E mutant polypeptide. The flt3-L protein | |
| CC | binds cell surface tyrosine kinase receptors and regulate growth and | |
| CC | differentiation of hematopoietic progenitor cells. The flt3-L protein can | |
| CC | be used to induce cellular expansion (especially in vivo) or | |
| CC | differentiation, e.g. in hematopoietic, natural killer (NK) or dendritic | |
| CC | cells, especially in the presence of growth factors such as interleukins, | |
| CC | colony stimulating factors or protein kinases. The protein can also | |
| CC | modulate, augment or enhance a patient's immune response and can be used | |
| CC | to treat an immune disorder (e.g. allergy, autoimmunity or | |
| CC | immunosuppression). The protein may be used to treat a pathological | |
| CC | condition e.g. myelodysplasia, aplastic anemia, HIV infection, breast, | |
| CC | small cell lung, testicular or ovarian cancer, lymphoma, multiple | |
| CC | myeloma, neuroblastoma or acute leukemia. | |
| XX | | |
| XX | Sequence | 209 AA; |
| XX | | |
| XX | Query Match | 89.4%; Score 1110; DB 21; Length 209; |
| XX | Best Local Similarity | 99.5%; Pred. No. 1.2e-96; |
| XX | Matches 208; Conservative | 1; Mismatches 0; Indels 0; Gaps 0 |
| QY | 27 | TQDCSFQHSPISSDFAVKIRIELSDLLQDYPYTVASNLQDEELCGIMFLVLAQRMERL 86 |
| DB | 1 | TQDCSFQHSPISSDFAVKIRIELSDLLQDYPYTVASNLQDEELCGIMFLVLAQRMERL 60 |
| QY | 87 | KTVAGSKMOGLLERVNEIHFVTKCAFQPPSCIEFVQTNISRLLQETSEQLVAKPWIT 146 |
| DB | 61 | KTVAGSKMOGLLERVNEIHFVTECAFQPPSCIEFVQTNISRLLQETSEQLVAKPWIT 120 |
| QY | 147 | RQNSRCELEQCCDDSSLRPPWSRPLQEARPTAPQPPRLILLLLPVGLILLAAKCLH 206 |

CC myeloma, neuroblastoma or acute leukemia.
 XX Sequence 209 AA: 89.4%; Score 1110; DB 21; Length 209;
 SQ Best Local Similarity 99.5%; Pred. No. 1.2e-96;
 Query Match 0; Mismatches 1; Indels 0; Gaps 0;
 Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

27 TDDCSFQHSPISSDFAVKIRELSYLLQDYPYVNASNLODELCGLWRLVLAQRMERL 86
 DB 1 TDDCSFQHSPISSDFAVKIRELSYLLQDYPYVNASNLODELCGLWRLVLAQRMERL 60

QY 87 KTVAGSKMOGLLERVNTIEHFVTKCAFOPPSCLRFVOTNISRLLOETSEQLVALKPWIT 146
 DB 61 KTVAGSKMOGLLERVNTIEHFVTKCAFOPPSCLRFVOTNISRLLOETSEQLVALKPWIT 120

QY 147 RQNFSCLELQCCPDSSSTLPPWSPRPLEATAPAPQPELLLLLPVGLLLAAACMLH 206
 DB 121 RQNFSCLELQCCPDSSSTLPPWSPRPLEATAPAPQPELLLLLPVGLLLAAACMLH 180

QY 207 WQTRRRTPRPEQVPPVPSPODLLVEH 235
 DB 181 WQTRRRTPRPEQVPPVPSPODLLVEH 209

RESULT 14
 AAY69729 standard; Protein: 209 AA.

AC AAY69729;
 DT 05-JUL-2000 (first entry)
 DE Human flt-3 muteln A64T.

XX Immunomodulator; immunosuppressive; cytostatic; antianemic; anti-HIV;
 KM neutroprotective; antiallergic; flt3 ligand; flt3-L; wild type; allergy;
 KM cell surface tyrosine kinase receptor; hematopoietic progenitor cell;
 KM cellular expansion; cellular differentiation; natural killer cell;
 KM cancer; dendritic cell; immune response; autoimmunity; immunosuppression;
 KM myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;
 KM multiple myeloma; leukemia; muteln.

OS Homo sapiens.
 OS Synthetic.
 PN WO200001823-A2.
 XX 13-JAN-2000.
 PD 25-JUN-1999; 99MO-US14296.
 PF 02-JUL-1998; 98US-0109100.
 PR (IMMV) IMMUNEX CORP.
 PA Graddis TJ, McGrew JT;
 PI WPI: 2000-182115/16.
 DR Mutant soluble flt3 ligand polypeptide used in cellular expansion,
 PT immune response stimulation or treatment of pathological conditions,
 PT contains amino acid substitutions at positions 8, 84, 118 or 122
 XX Claim 13; Page 78-79; 90pp; English.

CC The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides
 CC which exhibits increased or decreased biological activity relative to
 CC the full length wild type (AAY69719) or mature (AAY69720) flt3-L
 CC polypeptides. This sequence represents an example of the novel flt3
 CC ligands and comprises the L26F mutant polypeptide. The flt3-L protein
 CC binds cell surface tyrosine kinase receptors and regulate growth and
 CC differentiation of hematopoietic progenitor cells. The flt3-L protein can

CC be used to induce cellular expansion (especially in vivo) or
 CC differentiation, e.g. in hematopoietic, natural killer (NK) or dendritic
 CC cells, especially in the presence of growth factors such as interleukins.
 CC colony stimulating factors or protein kinases. The protein can also
 CC modulate, augment or enhance a patient's immune response and can be used
 CC to treat an immune disorder (e.g. allergy, autoimmunity or
 CC immunosuppression). The protein may be used to treat a pathological
 CC condition e.g. myelodysplasia, aplastic anemia, HIV infection, breast,
 CC small cell lung, testicular or ovarian cancer, lymphoma, multiple
 CC myeloma, neuroblastoma or acute leukemia.

XX Sequence 209 AA: 89.4%; Score 1110; DB 21; Length 209;
 SQ Best Local Similarity 99.5%; Pred. No. 1.2e-96;
 Query Match 0; Mismatches 1; Indels 0; Gaps 0;
 Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

27 TDDCSFQHSPISSDFAVKIRELSYLLQDYPYVNASNLODELCGLWRLVLAQRMERL 86
 DB 1 TDDCSFQHSPISSDFAVKIRELSYLLQDYPYVNASNLODELCGLWRLVLAQRMERL 60

QY 87 KTVAGSKMOGLLERVNTIEHFVTKCAFOPPSCLRFVOTNISRLLOETSEQLVALKPWIT 146
 DB 61 KTVAGSKMOGLLERVNTIEHFVTKCAFOPPSCLRFVOTNISRLLOETSEQLVALKPWIT 120

QY 147 RQNFSCLELQCCPDSSSTLPPWSPRPLEATAPAPQPELLLLLPVGLLLAAACMLH 206
 DB 121 RQNFSCLELQCCPDSSSTLPPWSPRPLEATAPAPQPELLLLLPVGLLLAAACMLH 180

QY 207 WQTRRRTPRPEQVPPVPSPODLLVEH 235
 DB 181 WQTRRRTPRPEQVPPVPSPODLLVEH 209

RESULT 15
 AAY69722 standard; Protein: 209 AA.

AC AAY69722;
 DT 05-JUL-2000 (first entry)
 DE Human flt-3 muteln H8Y.

XX Immunomodulator; immunosuppressive; cytostatic; antianemic; anti-HIV;
 KM neutroprotective; antiallergic; flt3 ligand; flt3-L; wild type; allergy;
 KM cell surface tyrosine kinase receptor; hematopoietic progenitor cell;
 KM cellular expansion; cellular differentiation; natural killer cell;
 KM cancer; dendritic cell; immune response; autoimmunity; immunosuppression;
 KM myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;
 KM multiple myeloma; leukemia; muteln.

OS Homo sapiens.
 OS Synthetic.
 PN WO200001823-A2.
 XX 13-JAN-2000.
 PD 25-JUN-1999; 99MO-US14296.
 PF 02-JUL-1998; 98US-0109100.
 PR (IMMV) IMMUNEX CORP.
 PA Graddis TJ, McGrew JT;
 PI WPI: 2000-182115/16.
 DR Mutant soluble flt3 ligand polypeptide used in cellular expansion,
 PT immune response stimulation or treatment of pathological conditions,
 PT contains amino acid substitutions at positions 8, 84, 118 or 122
 XX

PS Claim 4; Page 81-82; 90pp; English.

XX The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides
CC which exhibits increased or decreased biological activity relative to
CC the full length wild type (AA69719) or mature (AA69720) flt3-L
CC polypeptides. This sequence represents an example of the novel flt-3
CC ligands and comprises the H87 mutant polypeptide. The flt3-L protein
CC binds cell surface tyrosine kinase receptors and regulate growth and
CC differentiation of hematopoietic progenitor cells. The flt3-L protein can
CC be used to induce cellular expansion (especially in vivo) or
CC differentiation, e.g. in hematopoietic, natural killer (NK) or dendritic
CC cells, especially in the presence of growth factors such as interleukins,
CC colony stimulating factors or protein kinases. The protein can also
CC modulate, augment or enhance a patient's immune response and can be used
CC to treat an immune disorder (e.g. allergy, autoimmunity or
CC immunosuppression). The protein may be used to treat a pathological
CC condition e.g. myelodysplasia, aplastic anemia, HIV infection, breast,
CC small cell lung, testicular or ovarian cancer, lymphoma, multiple
CC myeloma, neuroblastoma or acute leukemia.

XX
SQ Sequence 209 AA;

Query Match 89.2%; Score 1108; DB 21; Length 209;

Best Local Similarity 99.5%; Pred. No. 1.9e-96;
Matches 208; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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DB 1 TDCCSFQHSFISDFVAKIRELSDYLLQDIPVVASNLQDEELCGGLMRVLAQRMERL 60
QY 87 KTVAGSKMGLERVTETHEFTKCAFOPPSCGLRFYOTNISRLQETSQVLAQKRWIT 146
DB 61 KTVAGSKMGLERVTETHEFTKCAFOPPSCGLRFYOTNISRLQETSQVLAQKRWIT 120
QY 147 RQNFSLCLELQCCPDSSSTLPFPMSPPRLTAPAPQPLLLLLFPVGLLLAAACGLH 206
DB 121 RQNFSLCLELQCCPDSSSTLPFPMSPPRLTAPAPQPLLLLLFPVGLLLAAACGLH 180
QY 207 WQTRRRTRPRGQVPPVSPQDLLVEH 235
DB 181 WQTRRRTRPRGQVPPVSPQDLLVEH 209

Search completed: May 27, 2003, 18:27:13
Job time : 37 secs

GenCore version 5.1.4-p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 27, 2003, 18:28:06 ; Search time 57 Seconds
(without alignments)
408.870 Million cell updates/sec

Title: US-08-994-468-6

Perfect score: 1242
Sequence: 1 MTVLAPAWSPPTVLLLL...RPGQVPPSPQDLLVER 235

Scoring table:
BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 375593 seqs, 99172665 residues

Total number of hits satisfying chosen parameters: 375593

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 1 | 1242 | 100.0 | 235 | 9 | US-10-095-449-6 |
| 2 | 1242 | 100.0 | 235 | 10 | US-09-448-378-1 |
| 3 | 1242 | 100.0 | 235 | 10 | US-09-983-806-6 |
| 4 | 1242 | 100.0 | 235 | 10 | US-09-904-536-1 |
| 5 | 1124 | 89.7 | 202 | 10 | US-09-904-536-10 |
| 6 | 1114 | 89.7 | 202 | 10 | US-09-904-536-18 |
| 7 | 1110 | 89.4 | 209 | 10 | US-09-904-536-9 |
| 8 | 1110 | 89.4 | 209 | 10 | US-09-904-536-12 |
| 9 | 1110 | 89.4 | 209 | 10 | US-09-904-536-14 |
| 10 | 1110 | 89.4 | 209 | 10 | US-09-904-536-17 |
| 11 | 1108 | 89.2 | 209 | 10 | US-09-904-536-11 |
| 12 | 1108 | 89.2 | 209 | 10 | US-09-904-536-15 |
| 13 | 1107 | 89.1 | 209 | 10 | US-09-904-536-13 |
| 14 | 1106 | 89.0 | 209 | 10 | US-09-904-536-8 |
| 15 | 1100 | 88.6 | 209 | 10 | US-09-904-536-16 |
| 16 | 822 | 66.2 | 156 | 9 | US-10-053-355A-1 |
| 17 | 768.5 | 61.9 | 231 | 9 | US-10-095-449-2 |
| 18 | 768.5 | 61.9 | 231 | 10 | US-09-448-378-2 |
| 19 | 768.5 | 61.9 | 231 | 10 | US-09-983-806-2 |

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| 20 | 506.5 | 40.8 | 137 | 10 | US-09-904-536-19 | Sequence 19, Appl |
| 21 | 91.5 | 7.4 | 674 | 10 | US-09-899-471-2 | Sequence 2, Appl |
| 22 | 91.5 | 7.4 | 698 | 9 | US-09-866-050A-509 | Sequence 509, App |
| 23 | 91.5 | 7.4 | 698 | 9 | US-09-863-818A-8 | Sequence 8, Appl |
| 24 | 91.5 | 7.4 | 698 | 10 | US-09-899-471-5 | Sequence 5, Appl |
| 25 | 89.5 | 7.2 | 874 | 10 | US-09-826-508-26 | Sequence 26, Appl |
| 26 | 89.5 | 7.2 | 941 | 9 | US-09-793-139-47 | Sequence 47, Appl |
| 27 | 89.5 | 7.2 | 941 | 9 | US-10-300-616-31 | Sequence 31, Appl |
| 28 | 89.5 | 7.2 | 941 | 10 | US-09-818-879-47 | Sequence 47, Appl |
| 29 | 89.5 | 7.2 | 941 | 10 | US-09-211-755B-47 | Sequence 47, Appl |
| 30 | 88.5 | 7.1 | 1257 | 9 | US-10-109-324-2 | Sequence 2, Appl |
| 31 | 88 | 7.1 | 238 | 9 | US-10-174-363-30 | Sequence 30, Appl |
| 32 | 87.5 | 7.0 | 415 | 9 | US-09-917-372-20 | Sequence 20, Appl |
| 33 | 87.5 | 7.0 | 415 | 10 | US-09-826-212-6 | Sequence 6, Appl |
| 34 | 87.5 | 7.0 | 415 | 10 | US-09-907-372-20 | Sequence 20, Appl |
| 35 | 87.5 | 7.0 | 415 | 10 | US-09-935-727-8 | Sequence 8, Appl |
| 36 | 87.5 | 7.0 | 479 | 9 | US-10-108-605-57 | Sequence 57, Appl |
| 37 | 87.5 | 7.0 | 570 | 9 | US-09-991-996-104 | Sequence 104, App |
| 38 | 87.5 | 7.0 | 570 | 10 | US-09-874-923-104 | Sequence 104, App |
| 39 | 85.5 | 6.9 | 519 | 10 | US-09-925-300-1680 | Sequence 1680, Ap |
| 40 | 84.5 | 6.8 | 610 | 10 | US-09-783-708-1 | Sequence 1, Appl |
| 41 | 84.5 | 6.8 | 913 | 10 | US-09-223-490-4 | Sequence 4, Appl |
| 42 | 84.5 | 6.8 | 1134 | 9 | US-10-001-873-50 | Sequence 50, Appl |
| 43 | 84 | 6.8 | 107 | 10 | US-09-220-920-52 | Sequence 52, Appl |
| 44 | 84 | 6.8 | 220 | 9 | US-10-001-054-56 | Sequence 56, Appl |
| 45 | 84 | 6.8 | 220 | 10 | US-09-220-920-26 | Sequence 26, Appl |

ALIGNMENTS

RESULT 1
US-10-095-449-6
Sequence 6, Application US/10095449
Patent No. US20020160004A1

GENERAL INFORMATION:

APPLICANT: Lyman, Stewart D.

Beckmann, M. Patricia

TITLE OF INVENTION: Ligands for flk3/flk-2 Receptors

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: Stephen L. Malaska, Immunex Corporation

STREET: 51 University Street

CITY: Seattle

STATE: Washington

COUNTRY: US

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Macintosh

OPERATING SYSTEM: Macintosh 7.0.1

SOFTWARE: Microsoft Word, Version #5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/095,449

FILING DATE: 13-Mar-2002

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/669,692

FILING DATE: 24-JUN-1996

APPLICATION NUMBER: US/08/162,407

FILING DATE: December 3, 1993

APPLICATION NUMBER: 08/111,758

FILING DATE: August 25, 1993

APPLICATION NUMBER: 08/106,463

FILING DATE: August 12, 1993

APPLICATION NUMBER: 08/068,394

FILING DATE: May 24, 1993

ATTORNEY/AGENT INFORMATION:

NAME: Malaska, Stephen L.

REGISTRATION NUMBER: 32,655

REFERENCE/DOCKET NUMBER: 2813-C

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 587-0430

TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-095-449-6

Query Match 100.0%; Score 1242; DB 9; Length 235;
Best Local Similarity 100.0%; Pred. No. 1,4e-101;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MYVLAPAMSTYLLLLLSGLSGTDCSFQHSPISSDFAVKIRELSYLLQDYPTV 60
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DB 61 ASNLDEELCGGIMRLVLAORMERLKTVAAGSKMGLLEVNTEIHFVTKCAFOPPSCL 120
QY 121 REVQTNISRLQETSEQLVALKPWITRONFSRCLLEOCOPDSSSTLPMPSPRPLEATAPT 180
DB 121 REVQTNISRLQETSEQLVALKPWITRONFSRCLLEOCOPDSSSTLPMPSPRPLEATAPT 180
QY 181 APOPLLILLLLPVGLLLAAACLHMORTRRTPRPGEOVPVPSPODLLVEH 235
DB 181 APOPLLILLLLPVGLLLAAACLHMORTRRTPRPGEOVPVPSPODLLVEH 235

RESULT 2

US-09-448-378-1
Sequence 1, Application US/09448378
Patent No. US20020034517A1
GENERAL INFORMATION:
APPLICANT: Brasel, Kenneth
TITLE OF INVENTION: Dendritic Cell Stimulatory Factor
FILE REFERENCE: 2836-D
CURRENT APPLICATION NUMBER: US/09/448,378
CURRENT FILING DATE: 1999-11-23
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
LENGTH: 235
TYPE: PRT
ORGANISM: Homo sapiens
US-09-448-378-1

Query Match 100.0%; Score 1242; DB 10; Length 235;
Best Local Similarity 100.0%; Pred. No. 1,4e-101;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MYVLAPAMSTYLLLLLSGLSGTDCSFQHSPISSDFAVKIRELSYLLQDYPTV 60
QY 61 ASNLDEELCGGIMRLVLAORMERLKTVAAGSKMGLLEVNTEIHFVTKCAFOPPSCL 120
DB 61 ASNLDEELCGGIMRLVLAORMERLKTVAAGSKMGLLEVNTEIHFVTKCAFOPPSCL 120
QY 121 REVQTNISRLQETSEQLVALKPWITRONFSRCLLEOCOPDSSSTLPMPSPRPLEATAPT 180
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QY 181 APOPLLILLLLPVGLLLAAACLHMORTRRTPRPGEOVPVPSPODLLVEH 235
DB 181 APOPLLILLLLPVGLLLAAACLHMORTRRTPRPGEOVPVPSPODLLVEH 235

RESULT 3
US-09-983-806-6

Sequence 6, Application US/09983806
Patent No. US20020107365A1
GENERAL INFORMATION:
APPLICANT: Lyman, Stewart D.
TITLE OF INVENTION: Ligands for f1t3/f1k-2 Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephen L. Malaska, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0.1
SOFTWARE: Microsoft Word, Version #5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/983,806
FILING DATE: 25-Oct-2001
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/444,626
FILING DATE: 19-MAY-1995
APPLICATION NUMBER: US 08/162,407
FILING DATE: 03-DEC-1993
APPLICATION NUMBER: 08/111,758
FILING DATE: August 25, 1993
APPLICATION NUMBER: 08/106,463
FILING DATE: August 12, 1993
APPLICATION NUMBER: 08/068,394
FILING DATE: May 24, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 2813-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-983-806-6

Query Match 100.0%; Score 1242; DB 10; Length 235;
Best Local Similarity 100.0%; Pred. No. 1,4e-101;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 ASNLDEELCGGIMRLVLAORMERLKTVAAGSKMGLLEVNTEIHFVTKCAFOPPSCL 120
QY 121 REVQTNISRLQETSEQLVALKPWITRONFSRCLLEOCOPDSSSTLPMPSPRPLEATAPT 180
DB 121 REVQTNISRLQETSEQLVALKPWITRONFSRCLLEOCOPDSSSTLPMPSPRPLEATAPT 180
QY 181 APOPLLILLLLPVGLLLAAACLHMORTRRTPRPGEOVPVPSPODLLVEH 235
DB 181 APOPLLILLLLPVGLLLAAACLHMORTRRTPRPGEOVPVPSPODLLVEH 235

RESULT 4

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US-09-904-536-1
; Sequence 1, Application US/09904536
; Patent No. US2002011475A1
; GENERAL INFORMATION:
; APPLICANT: McGraw, Thomas J.
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
; FILE REFERENCE: 03260.0028
; CURRENT APPLICATION NUMBER: US/09/904,536
; PRIOR FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 235
; TYPE: PRN
; ORGANISM: Homo sapiens
US-09-904-536-1
Query Match          100.0%; Score 1242; DB 10; Length 235;
Best Local Similarity 100.0%; Pred. No. 1.4e-101;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 ASNLODEELCGMLRVLAQRMERLKTAVAGSKMOGLLERVTEIHFTVKCAFQPPSCL 120
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DB 181 APOPPRLLLLPVGLLLAAAMCLHMOTRRRTPRRGQVPPVSPDOLLVEH 235

RESULT 5
US-09-904-536-10
; Sequence 10, Application US/09904536
; Patent No. US2002011475A1
; GENERAL INFORMATION:
; APPLICANT: McGraw, Thomas J.
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
; FILE REFERENCE: 03260.0028
; CURRENT APPLICATION NUMBER: US/09/904,536
; PRIOR FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 10
; LENGTH: 212
; TYPE: PRN
; ORGANISM: Homo sapiens
US-09-904-536-10
Query Match          90.5%; Score 1124; DB 10; Length 212;
Best Local Similarity 100.0%; Pred. No. 3e-91;
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 2 SGTODCSFQHSPISSDFAVKIRELSDYLLQDYPVTYASNLQDEELCGMLRVLAQRMER 84
QY 85 RLKTVAGSKMOGLLERVTEIHFTVKCAFQPPSCLRFVQTNISRLQETSSEQVALKAP 144
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DB 62 RLKTVAGSKMOGLLERVTEIHFTVKCAFQPPSCLRFVQTNISRLQETSSEQVALKAP 121
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QY 145 ITRONFSCLELQCCPDSSSTLPPWSPRPLEATPTAPOPPLLLLLPVGLLLAAAMC 204
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DB 122 ITRONFSCLELQCCPDSSSTLPPWSPRPLEATPTAPOPPLLLLLPVGLLLAAAMC 181
QY 205 LHMOTRRRTPRRGQVPPVSPDOLLVEH 235
    |||||||
DB 182 LHMOTRRRTPRRGQVPPVSPDOLLVEH 212

RESULT 6
US-09-904-536-18
; Sequence 18, Application US/09904536
; Patent No. US2002011475A1
; GENERAL INFORMATION:
; APPLICANT: McGraw, Thomas J.
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
; FILE REFERENCE: 03260.0028
; CURRENT APPLICATION NUMBER: US/09/904,536
; PRIOR FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 18
; LENGTH: 209
; TYPE: PRN
; ORGANISM: Homo sapiens
US-09-904-536-18
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Best Local Similarity 100.0%; Pred. No. 2.2e-90;
Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 TQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTYASNLQDEELCGMLRVLAQRMERL 60
QY 87 KTVAGSKMOGLLERVTEIHFTVKCAFQPPSCLRFVQTNISRLQETSSEQVALKAPWIT 146
    |||||||
DB 61 KTVAGSKMOGLLERVTEIHFTVKCAFQPPSCLRFVQTNISRLQETSSEQVALKAPWIT 120
QY 147 RQNFSCLELQCCPDSSSTLPPWSPRPLEATPTAPOPPLLLLLPVGLLLAAAMC 206
    |||||||
DB 121 RQNFSCLELQCCPDSSSTLPPWSPRPLEATPTAPOPPLLLLLPVGLLLAAAMC 180
QY 207 WQTRRRTPRGQVPPVSPDOLLVEH 235
    |||||||
DB 181 WQTRRRTPRGQVPPVSPDOLLVEH 209

RESULT 7
US-09-904-536-9
; Sequence 9, Application US/09904536
; Patent No. US2002011475A1
; GENERAL INFORMATION:
; APPLICANT: McGraw, Thomas J.
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
; FILE REFERENCE: 03260.0028
; CURRENT APPLICATION NUMBER: US/09/904,536
; PRIOR FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 9
; LENGTH: 209
; TYPE: PRN
; ORGANISM: Homo sapiens
US-09-904-536-9
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Query Match      89.4%; Score 1110; DB 10; Length 209;
Best Local Similarity 99.5%; Pred. No. 5e-90;
Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 27 TODCSFQHSPISSDFAVKIRELSYLLQDYPTVASNLODEELCGGLRWLVLAQRMERL 86
DB 1 TODCSFQHSPISSDFAVKIRELSYLLQDYPTVASNLODEELCGGLRWLVLAQRMERL 60
QY 87 KTVAGSKMOGLLEERVNTEIHFVTKCAFQPPSCLEFVQTNISRLQETSEQVALKPWIT 146
DB 61 KTVAGSKMOGLLEERVNTEIHFVTKCAFQPPSCLEFVQTNISRLQETSEQVALKPWIT 120
QY 147 RQNFSCLELOCOPDSSSTLPWPMSRPLEATAPTAQPPILLLLPVGLLLAAACMH 206
DB 121 RQNFSCLELOCOPDSSSTLPWPMSRPLEATAPTAQPPILLLLPVGLLLAAACMH 180
QY 207 WQTRRRTPRPGEOVPVPVSPQDLLVEH 235
DB 181 WQTRRRTPRPGEOVPVPVSPQDLLVEH 209

RESULT 8
US-09-904-536-12
; Sequence 12, Application US/09904536
; Patent No. US2002011475A1
; GENERAL INFORMATION:
; APPLICANT: Graddis, Thomas J.
; APPLICANT: McGrew, Jeffrey T.
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
; FILE REFERENCE: 03260.0028
; CURRENT APPLICATION NUMBER: US/09/904,536
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-904-536-12

Query Match      89.4%; Score 1110; DB 10; Length 209;
Best Local Similarity 99.5%; Pred. No. 5e-90;
Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 27 TODCSFQHSPISSDFAVKIRELSYLLQDYPTVASNLODEELCGGLRWLVLAQRMERL 86
DB 1 TODCSFQHSPISSDFAVKIRELSYLLQDYPTVASNLODEELCGGLRWLVLAQRMERL 60
QY 87 KTVAGSKMOGLLEERVNTEIHFVTKCAFQPPSCLEFVQTNISRLQETSEQVALKPWIT 146
DB 61 KTVAGSKMOGLLEERVNTEIHFVTKCAFQPPSCLEFVQTNISRLQETSEQVALKPWIT 120
QY 147 RQNFSCLELOCOPDSSSTLPWPMSRPLEATAPTAQPPILLLLPVGLLLAAACMH 206
DB 121 RQNFSCLELOCOPDSSSTLPWPMSRPLEATAPTAQPPILLLLPVGLLLAAACMH 180
QY 207 WQTRRRTPRPGEOVPVPVSPQDLLVEH 235
DB 181 WQTRRRTPRPGEOVPVPVSPQDLLVEH 209

RESULT 9
US-09-904-536-14
; Sequence 14, Application US/09904536
; Patent No. US2002011475A1
; GENERAL INFORMATION:
; APPLICANT: Graddis, Thomas J.
; APPLICANT: McGrew, Jeffrey T.
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
; FILE REFERENCE: 03260.0028
; CURRENT APPLICATION NUMBER: US/09/904,536

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; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-904-536-14

Query Match      89.4%; Score 1110; DB 10; Length 209;
Best Local Similarity 99.5%; Pred. No. 5e-90;
Matches 208; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 27 TODCSFQHSPISSDFAVKIRELSYLLQDYPTVASNLODEELCGGLRWLVLAQRMERL 86
DB 1 TODCSFQHSPISSDFAVKIRELSYLLQDYPTVASNLODEELCGGLRWLVLAQRMERL 60
QY 87 KTVAGSKMOGLLEERVNTEIHFVTKCAFQPPSCLEFVQTNISRLQETSEQVALKPWIT 146
DB 61 KTVAGSKMOGLLEERVNTEIHFVTKCAFQPPSCLEFVQTNISRLQETSEQVALKPWIT 120
QY 147 RQNFSCLELOCOPDSSSTLPWPMSRPLEATAPTAQPPILLLLPVGLLLAAACMH 206
DB 121 RQNFSCLELOCOPDSSSTLPWPMSRPLEATAPTAQPPILLLLPVGLLLAAACMH 180
QY 207 WQTRRRTPRPGEOVPVPVSPQDLLVEH 235
DB 181 WQTRRRTPRPGEOVPVPVSPQDLLVEH 209

RESULT 10
US-09-904-536-17
; Sequence 17, Application US/09904536
; Patent No. US2002011475A1
; GENERAL INFORMATION:
; APPLICANT: Graddis, Thomas J.
; APPLICANT: McGrew, Jeffrey T.
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
; FILE REFERENCE: 03260.0028
; CURRENT APPLICATION NUMBER: US/09/904,536
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-904-536-17

Query Match      89.4%; Score 1110; DB 10; Length 209;
Best Local Similarity 99.5%; Pred. No. 5e-90;
Matches 208; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 27 TODCSFQHSPISSDFAVKIRELSYLLQDYPTVASNLODEELCGGLRWLVLAQRMERL 86
DB 1 TODCSFQHSPISSDFAVKIRELSYLLQDYPTVASNLODEELCGGLRWLVLAQRMERL 60
QY 87 KTVAGSKMOGLLEERVNTEIHFVTKCAFQPPSCLEFVQTNISRLQETSEQVALKPWIT 146
DB 61 KTVAGSKMOGLLEERVNTEIHFVTKCAFQPPSCLEFVQTNISRLQETSEQVALKPWIT 120
QY 147 RQNFSCLELOCOPDSSSTLPWPMSRPLEATAPTAQPPILLLLPVGLLLAAACMH 206
DB 121 RQNFSCLELOCOPDSSSTLPWPMSRPLEATAPTAQPPILLLLPVGLLLAAACMH 180
QY 207 WQTRRRTPRPGEOVPVPVSPQDLLVEH 235
DB 181 WQTRRRTPRPGEOVPVPVSPQDLLVEH 209

```

RESULT 11
US-09-904-536-11
Sequence 11, Application US/09904536
Patent No. US2002011475A1
GENERAL INFORMATION:
APPLICANT: Graddis, Thomas J.
APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
FILE REFERENCE: 03260.0028
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: US/09/904,536
PRIOR FILING DATE: 1999-07-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 11
LENGTH: 209
TYPE: PRF
ORGANISM: Homo sapiens
US-09-904-536-11

Query Match 89.2%; Score 1108; DB 10; Length 209;
Best Local Similarity 99.5%; Pred. No. 7.4e-90;
Matches 208; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 27 TODCSFQHSPISSDFAVKIRELSYLLQDYPTVASNLQDEELCGGLMRLVLAQRMMERL 86
DB 1 TODCSFQHSPISSDFAVKIRELSYLLQDYPTVASNLQDEELCGGLMRLVLAQRMMERL 60
QY 87 KTVAGSKMOGLLEKRYNTEHFTVKCAFQPPSCLEFVQTNISRLQETSEQLVAAKPMIT 146
DB 61 KTVAGSKMOGLLEKRYNTEHFTVKCAFQPPSCLEFVQTNISRLQETSEQLVAAKPMIT 120
QY 147 RQNSRCLLEQCCOPDSSSTLPSPSPRPLEATAPAPQPLLLLLPVGLLLAAACMLH 206
DB 121 RQNSRCLLEQCCOPDSSSTLPSPSPRPLEATAPAPQPLLLLLPVGLLLAAACMLH 180
QY 207 WQTRRRTPRGEQVPPVPSQDILLVEH 235
DB 181 WQTRRRTPRGEQVPPVPSQDILLVEH 209

RESULT 12
US-09-904-536-15
Sequence 15, Application US/09904536
Patent No. US2002011475A1
GENERAL INFORMATION:
APPLICANT: Graddis, Thomas J.
APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
FILE REFERENCE: 03260.0028
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: US/09/904,536
PRIOR FILING DATE: 1999-07-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 15
LENGTH: 209
TYPE: PRF
ORGANISM: Homo sapiens
US-09-904-536-15

Query Match 89.2%; Score 1108; DB 10; Length 209;
Best Local Similarity 99.5%; Pred. No. 7.4e-90;
Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 27 TODCSFQHSPISSDFAVKIRELSYLLQDYPTVASNLQDEELCGGLMRLVLAQRMMERL 86
DB 1 TODCSFQHSPISSDFAVKIRELSYLLQDYPTVASNLQDEELCGGLMRLVLAQRMMERL 60
QY 87 KTVAGSKMOGLLEKRYNTEHFTVKCAFQPPSCLEFVQTNISRLQETSEQLVAAKPMIT 146

DB 61 KTVAGSKMOGLLEKRYNTEHFTVKCAFQPPSCLEFVQTNISRLQETSEQLVAAKPMIT 120
QY 147 RQNSRCLLEQCCOPDSSSTLPSPSPRPLEATAPAPQPLLLLLPVGLLLAAACMLH 206
DB 121 RQNSRCLLEQCCOPDSSSTLPSPSPRPLEATAPAPQPLLLLLPVGLLLAAACMLH 180
QY 207 WQTRRRTPRGEQVPPVPSQDILLVEH 235
DB 181 WQTRRRTPRGEQVPPVPSQDILLVEH 209

RESULT 13
US-09-904-536-13
Sequence 13, Application US/09904536
Patent No. US2002011475A1
GENERAL INFORMATION:
APPLICANT: Graddis, Thomas J.
APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
FILE REFERENCE: 03260.0028
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: US/09/904,536
PRIOR FILING DATE: 1999-07-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 13
LENGTH: 209
TYPE: PRF
ORGANISM: Homo sapiens
US-09-904-536-13

Query Match 89.1%; Score 1107; DB 10; Length 209;
Best Local Similarity 99.5%; Pred. No. 9.1e-90;
Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 27 TODCSFQHSPISSDFAVKIRELSYLLQDYPTVASNLQDEELCGGLMRLVLAQRMMERL 86
DB 1 TODCSFQHSPISSDFAVKIRELSYLLQDYPTVASNLQDEELCGGLMRLVLAQRMMERL 60
QY 87 KTVAGSKMOGLLEKRYNTEHFTVKCAFQPPSCLEFVQTNISRLQETSEQLVAAKPMIT 146
DB 61 KTVAGSKMOGLLEKRYNTEHFTVKCAFQPPSCLEFVQTNISRLQETSEQLVAAKPMIT 120
QY 147 RQNSRCLLEQCCOPDSSSTLPSPSPRPLEATAPAPQPLLLLLPVGLLLAAACMLH 206
DB 121 RQNSRCLLEQCCOPDSSSTLPSPSPRPLEATAPAPQPLLLLLPVGLLLAAACMLH 180
QY 207 WQTRRRTPRGEQVPPVPSQDILLVEH 235
DB 181 WQTRRRTPRGEQVPPVPSQDILLVEH 209

RESULT 14
US-09-904-536-8
Sequence 8, Application US/09904536
Patent No. US2002011475A1
GENERAL INFORMATION:
APPLICANT: Graddis, Thomas J.
APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
FILE REFERENCE: 03260.0028
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: US/09/904,536
PRIOR FILING DATE: 1999-07-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 8
LENGTH: 209
TYPE: PRF
ORGANISM: Homo sapiens

US-09-904-536-8

Query Match 89.0%; Score 1106; DB 10; Length 209;
Best Local Similarity 99.5%; Pred. No. 1.1e-89;
Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 27 TODCSFQHSPISSDFAVKIRELSYLDYLDYPTVYASNLODEELCGGLMRVLVLAORMERL 86
DB 1 TODCSFQHSPISSDFAVKIRELSYLDYLDYPTVYASNLODEELCGGLMRVLVLAORMERL 60
QY 87 KTVAGSKMOGLERVTETHEFTKCAFOPPPSCLRFVQTNISRLQETSEQLVALKPMIT 146
DB 61 KTVAGSKMOGLERVTETHEFTKCAFOPPPSCLRFVQTNISRLQETSEQLVALKPMIT 120
QY 147 RQNFSCLELOCOPDSSSTLPWPSPRPLEATAPAPOLLILLPVGILLAAACMH 206
DB 121 RQNFSCLELOCOPDSSSTLPWPSPRPLEATAPAPOLLILLPVGILLAAACMH 180
QY 207 WQTRRRTRPRGEQVPPVPSPODLLVEH 235
DB 181 WQTRRRTRPRGEQVPPVPSPODLLVEH 209

RESULT 15

US-09-904-536-16
Sequence 16, Application US/09904536
Patent No. US2002011475A1
GENERAL INFORMATION:
APPLICANT: Graddis, Thomas J.
APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
FILE REFERENCE: 03260.0028
CURRENT APPLICATION NUMBER: US/09/904,536
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100
PRIOR FILING DATE: 1999-07-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 16
LENGTH: 209
TYPE: PRT
ORGANISM: Homo sapiens
US-09-904-536-16

Query Match 88.6%; Score 1100; DB 10; Length 209;
Best Local Similarity 99.5%; Pred. No. 3.8e-89;
Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 27 TODCSFQHSPISSDFAVKIRELSYLDYLDYPTVYASNLODEELCGGLMRVLVLAORMERL 86
DB 1 TODCSFQHSPISSDFAVKIRELSYLDYLDYPTVYASNLODEELCGGLMRVLVLAORMERL 60
QY 87 KTVAGSKMOGLERVTETHEFTKCAFOPPPSCLRFVQTNISRLQETSEQLVALKPMIT 146
DB 61 KTVAGSKMOGLERVTETHEFTKCAFOPPPSCLRFVQTNISRLQETSEQLVALKPMIT 120
QY 147 RQNFSCLELOCOPDSSSTLPWPSPRPLEATAPAPOLLILLPVGILLAAACMH 206
DB 121 RQNFSCLELOCOPDSSSTLPWPSPRPLEATAPAPOLLILLPVGILLAAACMH 180
QY 207 WQTRRRTRPRGEQVPPVPSPODLLVEH 235
DB 181 WQTRRRTRPRGEQVPPVPSPODLLVEH 209

Search completed: May 27, 2003, 18:36:27
Job time : 58 secs

GenCore version 5.1.4-p5-4578
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OM protein - protein search, using sw model

Run on: May 27, 2003, 18:26:36 ; Search time 15 Seconds

(without alignments)
460.959 Million cell updates/sec

Title: US-08-994-468-6

Perfect score: 1242
Sequence: 1 MTVALPAMSPFTYLLLLLL.....RPGGVVPPVPSQDLLLVH 235

Scoring table: BLOSUM62

Searched: Gap0 10.0 , Gapext 0.5
262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: /cgn2-6/ptodata/1/aa/5A.COMB.pep:*
2: /cgn2-6/ptodata/1/aa/5B.COMB.pep:*
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4: /cgn2-6/ptodata/1/aa/6B.COMB.pep:*
5: /cgn2-6/ptodata/1/aa/PCTUS.COMB.pep:*
6: /cgn2-6/ptodata/1/aa/Backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|---------------------|-------------------|
| 1 | 1242 | 100.0 | 235 | 1 US-08-243-545-6 | Sequence 6, Appl |
| 2 | 1242 | 100.0 | 235 | 2 US-08-993-962-6 | Sequence 6, Appl |
| 3 | 1242 | 100.0 | 235 | 4 US-09-160-841-6 | Sequence 6, Appl |
| 4 | 1242 | 100.0 | 235 | 4 US-09-109-100-1 | Sequence 1, Appl |
| 5 | 1242 | 100.0 | 235 | 5 PCT-US94-05365-6 | Sequence 6, Appl |
| 6 | 1124 | 90.5 | 212 | 4 US-09-109-100-10 | Sequence 10, Appl |
| 7 | 1114 | 89.7 | 209 | 4 US-09-109-100-18 | Sequence 18, Appl |
| 8 | 1110 | 89.4 | 209 | 4 US-09-109-100-9 | Sequence 9, Appl |
| 9 | 1110 | 89.4 | 209 | 4 US-09-109-100-12 | Sequence 12, Appl |
| 10 | 1110 | 89.4 | 209 | 4 US-09-109-100-14 | Sequence 14, Appl |
| 11 | 1110 | 89.4 | 209 | 4 US-09-109-100-17 | Sequence 17, Appl |
| 12 | 1108 | 89.2 | 209 | 4 US-09-109-100-11 | Sequence 11, Appl |
| 13 | 1108 | 89.2 | 209 | 4 US-09-109-100-15 | Sequence 15, Appl |
| 14 | 1107 | 89.1 | 209 | 4 US-09-109-100-13 | Sequence 13, Appl |
| 15 | 1106 | 89.0 | 209 | 4 US-09-109-100-8 | Sequence 8, Appl |
| 16 | 1100 | 88.6 | 209 | 4 US-09-109-100-16 | Sequence 16, Appl |
| 17 | 768.5 | 61.9 | 231 | 1 US-08-243-545-2 | Sequence 2, Appl |
| 18 | 768.5 | 61.9 | 231 | 2 US-08-993-962-2 | Sequence 2, Appl |
| 19 | 768.5 | 61.9 | 231 | 4 US-09-160-841-2 | Sequence 2, Appl |
| 20 | 768.5 | 61.9 | 231 | 5 PCT-US94-05365-2 | Sequence 2, Appl |
| 21 | 765.5 | 61.6 | 231 | 1 US-08-220-3798-7 | Sequence 7, Appl |
| 22 | 765.5 | 61.6 | 231 | 5 PCT-US95-03866-6 | Sequence 6, Appl |
| 23 | 506.5 | 40.8 | 137 | 4 US-09-109-100-19 | Sequence 19, Appl |
| 24 | 154 | 12.4 | 42 | 5 PCT-US94-05150-17 | Sequence 17, Appl |
| 25 | 91.5 | 7.4 | 675 | 1 US-08-317-522A-9 | Sequence 9, Appl |
| 26 | 91.5 | 7.4 | 675 | 1 US-08-439-818A-9 | Sequence 9, Appl |
| 27 | 91.5 | 7.4 | 675 | 2 US-08-751-965-9 | Sequence 9, Appl |

| | | | | | | |
|----|------|-----|-----|---|-------------------|-------------------|
| 28 | 91.5 | 7.4 | 675 | 2 | US-08-738-975-9 | Sequence 9, Appl |
| 29 | 91.5 | 7.4 | 675 | 2 | US-08-728-626-9 | Sequence 9, Appl |
| 30 | 91.5 | 7.4 | 675 | 3 | US-08-808-599A-9 | Sequence 9, Appl |
| 31 | 87.5 | 7.0 | 415 | 4 | US-09-006-353A-6 | Sequence 6, Appl |
| 32 | 87.5 | 7.0 | 415 | 4 | US-09-573-986-6 | Sequence 6, Appl |
| 33 | 85 | 6.8 | 366 | 1 | US-08-004-992-8 | Sequence 8, Appl |
| 34 | 84.5 | 6.8 | 913 | 1 | US-08-445-640-4 | Sequence 4, Appl |
| 35 | 84.5 | 6.8 | 913 | 3 | US-08-170-558-4 | Sequence 4, Appl |
| 36 | 84.5 | 6.8 | 913 | 3 | US-08-447-314-4 | Sequence 4, Appl |
| 37 | 84.5 | 6.8 | 107 | 4 | US-08-445-661-4 | Sequence 4, Appl |
| 38 | 84 | 6.8 | 107 | 4 | US-09-220-528-52 | Sequence 52, Appl |
| 39 | 84 | 6.8 | 220 | 4 | US-09-220-528-26 | Sequence 26, Appl |
| 40 | 83.5 | 6.7 | 429 | 1 | US-07-964-589-2 | Sequence 2, Appl |
| 41 | 83.5 | 6.7 | 429 | 5 | PCT-US93-02024-2 | Sequence 2, Appl |
| 42 | 83.5 | 6.7 | 671 | 3 | US-09-121-321-16 | Sequence 16, Appl |
| 43 | 83.5 | 6.7 | 671 | 4 | US-08-933-803A-16 | Sequence 16, Appl |
| 44 | 83 | 6.7 | 28 | 5 | PCT-US94-05150-12 | Sequence 12, Appl |
| 45 | 83 | 6.7 | 758 | 1 | US-07-756-250-16 | Sequence 16, Appl |

ALIGNMENTS

RESULT 1
US-08-243-545-6
Sequence 6, Application US/08243545
Patent No. 5554512
GENERAL INFORMATION:
APPLICANT: Lyman, Stewart D.
TITLE OR INVENTION: Ligands for fli3/fliK-2 Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephen L. Malaska, Immunex Corporation
STREET: 51 University Street
City: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0.1
SOFTWARE: Microsoft Word, Version #5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/243,545
FILING DATE: 11-May-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/162,407
FILING DATE: 03-DEC-1993
APPLICATION NUMBER: 08/111,758
FILING DATE: August 25, 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/106,463
FILING DATE: August 12, 1993
CLASSIFICATION: 435
APPLICATION DATA:
APPLICATION NUMBER: 08/068,394
FILING DATE: May 24, 1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 2813-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ. ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-243-545-6

Query Match 100.0%; Score 1242; DB 1; Length 235;
Best Local Similarity 100.0%; Pred. No. 1.7e-117;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVLAPAMSPPTTYLLLLSSGLSGTDCSFQSPISDFAVKIRELSDYLLQDYPV 60
DB 1 MVLAPAMSPPTTYLLLLSSGLSGTDCSFQSPISDFAVKIRELSDYLLQDYPV 60
QY 61 ASNIDEELCGGLWRLVLAORMERLKTAVAGSKMGLLEERVNTEIHFTVKCAFQPPSCL 120
DB 61 ASNIDEELCGGLWRLVLAORMERLKTAVAGSKMGLLEERVNTEIHFTVKCAFQPPSCL 120
QY 121 RFVOTNISRLQETSEQLVALKPWITRONFSRCLQCPDSSSTLPWPSPRLERATPT 180
DB 121 RFVOTNISRLQETSEQLVALKPWITRONFSRCLQCPDSSSTLPWPSPRLERATPT 180
QY 181 APOPELLLLLPVGLLLAAWCLHMQRTRRRPRPEQVPPVPSPODLLLVEH 235
DB 181 APOPELLLLLPVGLLLAAWCLHMQRTRRRPRPEQVPPVPSPODLLLVEH 235

RESULT 2
US-08-993-962-6
Sequence 6, Application US/08993962
Patent No. 5843423

GENERAL INFORMATION:

APPLICANT: Lyman, Stewart D.
APPLICANT: Beckmann, M. Patricia
TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephen L. Malaska, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0.1
SOFTWARE: Microsoft Word, Version #5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/993,962
FILING DATE: December 18, 1993
CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/162,407
FILING DATE: December 3, 1993
APPLICATION NUMBER: 08/111,758
FILING DATE: August 25, 1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/106,463
FILING DATE: August 12, 1993
CLASSIFICATION: 424
APPLICATION NUMBER: 08/068,394
FILING DATE: May 24, 1993

ATTORNEY/AGENT INFORMATION:

NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 2813-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822

INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-993-962-6

Query Match 100.0%; Score 1242; DB 2; Length 235;
Best Local Similarity 100.0%; Pred. No. 1.7e-117;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVLAPAMSPPTTYLLLLSSGLSGTDCSFQSPISDFAVKIRELSDYLLQDYPV 60
DB 1 MVLAPAMSPPTTYLLLLSSGLSGTDCSFQSPISDFAVKIRELSDYLLQDYPV 60
QY 61 ASNIDEELCGGLWRLVLAORMERLKTAVAGSKMGLLEERVNTEIHFTVKCAFQPPSCL 120
DB 61 ASNIDEELCGGLWRLVLAORMERLKTAVAGSKMGLLEERVNTEIHFTVKCAFQPPSCL 120
QY 121 RFVOTNISRLQETSEQLVALKPWITRONFSRCLQCPDSSSTLPWPSPRLERATPT 180
DB 121 RFVOTNISRLQETSEQLVALKPWITRONFSRCLQCPDSSSTLPWPSPRLERATPT 180
QY 181 APOPELLLLLPVGLLLAAWCLHMQRTRRRPRPEQVPPVPSPODLLLVEH 235
DB 181 APOPELLLLLPVGLLLAAWCLHMQRTRRRPRPEQVPPVPSPODLLLVEH 235

RESULT 3
US-09-160-841-6
Sequence 6, Application US/09160841
Patent No. 6190655

GENERAL INFORMATION:

APPLICANT: Lyman, Stewart D.
APPLICANT: Beckmann, M. Patricia
TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephen L. Malaska, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0.1
SOFTWARE: Microsoft Word, Version #5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/160,841
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/162,407
FILING DATE: December 3, 1993
APPLICATION NUMBER: 08/111,758
FILING DATE: August 25, 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/106,463
FILING DATE: August 12, 1993
APPLICATION NUMBER: 08/068,394
FILING DATE: May 24, 1993

ATTORNEY/AGENT INFORMATION:

NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 2813-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822

INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-160-841-6

Query Match 100.0%; Score 1242; DB 4; Length 235;
Best Local Similarity 100.0%; Pred. No. 1.7e-117;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVLAPAMSPPTTYLLLLSSGLSGTDCSFQHSPISSDPAVKIRELSDYLLQDYPVTY 60
DB 1 MTVLAPAMSPPTTYLLLLSSGLSGTDCSFQHSPISSDPAVKIRELSDYLLQDYPVTY 60
QY 61 ASNLQDEELCGGLMRLVLAQRMERLKTVAAGSKMGLLERYNTEIHFTKCAFOPPPSCL 120
DB 61 ASNLQDEELCGGLMRLVLAQRMERLKTVAAGSKMGLLERYNTEIHFTKCAFOPPPSCL 120
QY 121 RFVQTNISRLQETSEQLVAKPMTTRQNFRCLELQCPDSSSTLPWPSPRPLEATAPT 180
DB 121 RFVQTNISRLQETSEQLVAKPMTTRQNFRCLELQCPDSSSTLPWPSPRPLEATAPT 180
QY 181 APOPLLILLPLVGLLLAAACLMQRTRRTPRGEQVPVPSPODLLLVEH 235
DB 181 APOPLLILLPLVGLLLAAACLMQRTRRTPRGEQVPVPSPODLLLVEH 235

RESULT 4
US-09-109-100-1
Sequence 1, Application US/09109100C
Patent No. 6291661

GENERAL INFORMATION:
APPLICANT: Gradis, Thomas J.
APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
FILE REFERENCE: 03260.0028
CURRENT APPLICATION NUMBER: US/09/109,100C
CURRENT FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 235
TYPE: PRT
ORGANISM: Homo sapiens
US-09-109-100-1

Query Match 100.0%; Score 1242; DB 4; Length 235;
Best Local Similarity 100.0%; Pred. No. 1.7e-117;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVLAPAMSPPTTYLLLLSSGLSGTDCSFQHSPISSDPAVKIRELSDYLLQDYPVTY 60
DB 1 MTVLAPAMSPPTTYLLLLSSGLSGTDCSFQHSPISSDPAVKIRELSDYLLQDYPVTY 60
QY 61 ASNLQDEELCGGLMRLVLAQRMERLKTVAAGSKMGLLERYNTEIHFTKCAFOPPPSCL 120
DB 61 ASNLQDEELCGGLMRLVLAQRMERLKTVAAGSKMGLLERYNTEIHFTKCAFOPPPSCL 120
QY 121 RFVQTNISRLQETSEQLVAKPMTTRQNFRCLELQCPDSSSTLPWPSPRPLEATAPT 180
DB 121 RFVQTNISRLQETSEQLVAKPMTTRQNFRCLELQCPDSSSTLPWPSPRPLEATAPT 180
QY 181 APOPLLILLPLVGLLLAAACLMQRTRRTPRGEQVPVPSPODLLLVEH 235
DB 181 APOPLLILLPLVGLLLAAACLMQRTRRTPRGEQVPVPSPODLLLVEH 235

RESULT 5
PCT-US94-05365-6
Sequence 6, Application PC/TUS9405365
GENERAL INFORMATION:

APPLICANT: Lyman, Stewart D.
APPLICANT: Beckmann, M. Patricia
TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephen L. Malaska, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/05365
FILING DATE: May 24, 1994

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: -to be assigned-
FILING DATE: May 11, 1994

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/209,502
FILING DATE: March 7, 1994

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/162,407
FILING DATE: December 3, 1993

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/111,758
FILING DATE: August 25, 1993

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/106,463
FILING DATE: August 12, 1993

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/068,394
FILING DATE: May 24, 1993

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Malaska, Stephen L.

REGISTRATION NUMBER: 32,655

REFERENCE/DOCKET NUMBER: 2813-B

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 587-0430

TELEFAX: (206) 233-0644

TELEX: 756822

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 235 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein
PCT-US94-05365-6

Query Match 100.0%; Score 1242; DB 5; Length 235;
Best Local Similarity 100.0%; Pred. No. 1.7e-117;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVLAPAMSPPTTYLLLLSSGLSGTDCSFQHSPISSDPAVKIRELSDYLLQDYPVTY 60
DB 1 MTVLAPAMSPPTTYLLLLSSGLSGTDCSFQHSPISSDPAVKIRELSDYLLQDYPVTY 60
QY 61 ASNLQDEELCGGLMRLVLAQRMERLKTVAAGSKMGLLERYNTEIHFTKCAFOPPPSCL 120
DB 61 ASNLQDEELCGGLMRLVLAQRMERLKTVAAGSKMGLLERYNTEIHFTKCAFOPPPSCL 120
QY 121 RFVQTNISRLQETSEQLVAKPMTTRQNFRCLELQCPDSSSTLPWPSPRPLEATAPT 180


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Query Match      89.4%; Score 1110; DB 4; Length 209;
Best Local Similarity 99.5%; Pred. No. 3e-104;
Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 27 TODCSFQHSPISSDFAVKIRELSIDYLDYPTVASNLODEELCGGLMRLVLAORMERL 86
DB 1 TODCSFQHSPISSDFAVKIRELSIDYLDYPTVASNLODEELCGGLMRLVLAORMERL 60

QY 87 KTVAGSKMOGLLERVNTIEHFVTKCAFOPPPSCLRFVOTNISRLLOETSEQVALKPMIT 146
DB 61 KTVAGSKMOGLLERVNTIEHFVTKCAFOPPPSCLRFVOTNISRLLOETSEQVALKPMIT 120

QY 147 RQNFSCLELOCOPDSSSTLPMPSPRPLEATAPAPOPPLLLLLPVGLLLAAACMLH 206
DB 121 RQNFSCLELOCOPDSSSTLPMPSPRPLEATAPAPOPPLLLLLPVGLLLAAACMLH 180

QY 207 WQTRRRTRPRGEOVPPVPSPODLLVEH 235
DB 181 WQTRRRTRPRGEOVPPVPSPODLLVEH 209

RESULT 10
US-09-109-100-14
Sequence 14, Application US/09109100C
Patent No. 6291661
GENERAL INFORMATION:
APPLICANT: McGraw, Thomas J.
APPLICANT: McGraw, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
FILE REFERENCE: 03260.0028
CURRENT APPLICATION NUMBER: US/09/109,100C
CURRENT FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 14
LENGTH: 209
TYPE: PRT
ORGANISM: Homo sapiens
US-09-109-100-14

Query Match      89.4%; Score 1110; DB 4; Length 209;
Best Local Similarity 99.5%; Pred. No. 3e-104;
Matches 208; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 27 TODCSFQHSPISSDFAVKIRELSIDYLDYPTVASNLODEELCGGLMRLVLAORMERL 86
DB 1 TODCSFQHSPISSDFAVKIRELSIDYLDYPTVASNLODEELCGGLMRLVLAORMERL 60

QY 87 KTVAGSKMOGLLERVNTIEHFVTKCAFOPPPSCLRFVOTNISRLLOETSEQVALKPMIT 146
DB 61 KTVAGSKMOGLLERVNTIEHFVTKCAFOPPPSCLRFVOTNISRLLOETSEQVALKPMIT 120

QY 147 RQNFSCLELOCOPDSSSTLPMPSPRPLEATAPAPOPPLLLLLPVGLLLAAACMLH 206
DB 121 RQNFSCLELOCOPDSSSTLPMPSPRPLEATAPAPOPPLLLLLPVGLLLAAACMLH 180

QY 207 WQTRRRTRPRGEOVPPVPSPODLLVEH 235
DB 181 WQTRRRTRPRGEOVPPVPSPODLLVEH 209

RESULT 11
US-09-109-100-17
Sequence 17, Application US/09109100C
Patent No. 6291661
GENERAL INFORMATION:
APPLICANT: McGraw, Thomas J.
APPLICANT: McGraw, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
FILE REFERENCE: 03260.0028
CURRENT APPLICATION NUMBER: US/09/109,100C
CURRENT FILING DATE: 1998-07-02
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NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 17
LENGTH: 209
TYPE: PRT
ORGANISM: Homo sapiens
US-09-109-100-17

Query Match      89.4%; Score 1110; DB 4; Length 209;
Best Local Similarity 99.5%; Pred. No. 3e-104;
Matches 208; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 27 TODCSFQHSPISSDFAVKIRELSIDYLDYPTVASNLODEELCGGLMRLVLAORMERL 86
DB 1 TODCSFQHSPISSDFAVKIRELSIDYLDYPTVASNLODEELCGGLMRLVLAORMERL 60

QY 87 KTVAGSKMOGLLERVNTIEHFVTKCAFOPPPSCLRFVOTNISRLLOETSEQVALKPMIT 146
DB 61 KTVAGSKMOGLLERVNTIEHFVTKCAFOPPPSCLRFVOTNISRLLOETSEQVALKPMIT 120

QY 147 RQNFSCLELOCOPDSSSTLPMPSPRPLEATAPAPOPPLLLLLPVGLLLAAACMLH 206
DB 121 RQNFSCLELOCOPDSSSTLPMPSPRPLEATAPAPOPPLLLLLPVGLLLAAACMLH 180

QY 207 WQTRRRTRPRGEOVPPVPSPODLLVEH 235
DB 181 WQTRRRTRPRGEOVPPVPSPODLLVEH 209

RESULT 12
US-09-109-100-11
Sequence 11, Application US/09109100C
Patent No. 6291661
GENERAL INFORMATION:
APPLICANT: McGraw, Thomas J.
APPLICANT: McGraw, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
FILE REFERENCE: 03260.0028
CURRENT APPLICATION NUMBER: US/09/109,100C
CURRENT FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 11
LENGTH: 209
TYPE: PRT
ORGANISM: Homo sapiens
US-09-109-100-11

Query Match      89.2%; Score 1108; DB 4; Length 209;
Best Local Similarity 99.5%; Pred. No. 4.8e-104;
Matches 208; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 27 TODCSFQHSPISSDFAVKIRELSIDYLDYPTVASNLODEELCGGLMRLVLAORMERL 86
DB 1 TODCSFQHSPISSDFAVKIRELSIDYLDYPTVASNLODEELCGGLMRLVLAORMERL 60

QY 87 KTVAGSKMOGLLERVNTIEHFVTKCAFOPPPSCLRFVOTNISRLLOETSEQVALKPMIT 146
DB 61 KTVAGSKMOGLLERVNTIEHFVTKCAFOPPPSCLRFVOTNISRLLOETSEQVALKPMIT 120

QY 147 RQNFSCLELOCOPDSSSTLPMPSPRPLEATAPAPOPPLLLLLPVGLLLAAACMLH 206
DB 121 RQNFSCLELOCOPDSSSTLPMPSPRPLEATAPAPOPPLLLLLPVGLLLAAACMLH 180

QY 207 WQTRRRTRPRGEOVPPVPSPODLLVEH 235
DB 181 WQTRRRTRPRGEOVPPVPSPODLLVEH 209

RESULT 13
US-09-109-100-15
Sequence 15, Application US/09109100C
Patent No. 6291661
```

GENERAL INFORMATION:
APPLICANT: Graddis, Thomas J.
APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
FILE REFERENCE: 03260.0028
CURRENT APPLICATION NUMBER: US/09/109.100C
CURRENT FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 15
LENGTH: 209
TYPE: PRT
ORGANISM: Homo sapiens
US-09-109-100-15

Query Match 89.2%; Score 1108; DB 4; Length 209;
Best Local Similarity 99.5%; Pred. No. 4.8e-104;
Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 27 TQDCSFQHSPISSDFAVKIRELSYLLQDYPTVASNLODEELCGGLMRVLVAQRMERL 86
DB 1 TQDCSFQHSPISSDFAVKIRELSYLLQDYPTVASNLODEELCGGLMRVLVAQRMERL 60
QY 87 KTVAGSKMOGLLERVNTIEHFVTKCAFQPPSCLEFVQTNISRLLOETSEQVALKPMIT 146
DB 61 KTVAGSKMOGLLERVNTIEHFVTKCAFQPPSCLEFVQTNISRLLOETSEQVALKPMIT 120
QY 147 RQNFSCLELOCOPDSTLPPWSPRPLEATAPAPQPLLILLPVGLLLAAACMLH 206
DB 121 RQNFSCLELOCOPDSTLPPWSPRPLEATAPAPQPLLILLPVGLLLAAACMLH 180
QY 207 WQTRRRTPRPGQVPPVPSPODLLVEH 235
DB 181 WQTRRRTPRPGQVPPVPSPODLLVEH 209

RESULT 14

US-09-109-100-13
Sequence 13, Application US/09109100C
Patent No. 6291661
GENERAL INFORMATION:
APPLICANT: Graddis, Thomas J.
APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
FILE REFERENCE: 03260.0028
CURRENT APPLICATION NUMBER: US/09/109.100C
CURRENT FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 13
LENGTH: 209
TYPE: PRT
ORGANISM: Homo sapiens
US-09-109-100-13

Query Match 89.1%; Score 1107; DB 4; Length 209;
Best Local Similarity 99.5%; Pred. No. 6e-104;
Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 27 TQDCSFQHSPISSDFAVKIRELSYLLQDYPTVASNLODEELCGGLMRVLVAQRMERL 86
DB 1 TQDCSFQHSPISSDFAVKIRELSYLLQDYPTVASNLODEELCGGLMRVLVAQRMERL 60
QY 87 KTVAGSKMOGLLERVNTIEHFVTKCAFQPPSCLEFVQTNISRLLOETSEQVALKPMIT 146
DB 61 KTVAGSKMOGLLERVNTIEHFVTKCAFQPPSCLEFVQTNISRLLOETSEQVALKPMIT 120
QY 147 RQNFSCLELOCOPDSTLPPWSPRPLEATAPAPQPLLILLPVGLLLAAACMLH 206
DB 121 RQNFSCLELOCOPDSTLPPWSPRPLEATAPAPQPLLILLPVGLLLAAACMLH 180
QY 207 WQTRRRTPRPGQVPPVPSPODLLVEH 235
DB 181 WQTRRRTPRPGQVPPVPSPODLLVEH 209

DB 181 WQTRRRTPRPGQVPPVPSPODLLVEH 209

RESULT 15

US-09-109-100-8
Sequence 8, Application US/09109100C
Patent No. 6291661
GENERAL INFORMATION:
APPLICANT: Graddis, Thomas J.
APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
FILE REFERENCE: 03260.0028
CURRENT APPLICATION NUMBER: US/09/109.100C
CURRENT FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 8
LENGTH: 209
TYPE: PRT
ORGANISM: Homo sapiens
US-09-109-100-8

Query Match 89.0%; Score 1106; DB 4; Length 209;
Best Local Similarity 99.5%; Pred. No. 7.6e-104;
Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 27 TQDCSFQHSPISSDFAVKIRELSYLLQDYPTVASNLODEELCGGLMRVLVAQRMERL 86
DB 1 TQDCSFQHSPISSDFAVKIRELSYLLQDYPTVASNLODEELCGGLMRVLVAQRMERL 60
QY 87 KTVAGSKMOGLLERVNTIEHFVTKCAFQPPSCLEFVQTNISRLLOETSEQVALKPMIT 146
DB 61 KTVAGSKMOGLLERVNTIEHFVTKCAFQPPSCLEFVQTNISRLLOETSEQVALKPMIT 120
QY 147 RQNFSCLELOCOPDSTLPPWSPRPLEATAPAPQPLLILLPVGLLLAAACMLH 206
DB 121 RQNFSCLELOCOPDSTLPPWSPRPLEATAPAPQPLLILLPVGLLLAAACMLH 180
QY 207 WQTRRRTPRPGQVPPVPSPODLLVEH 235
DB 181 WQTRRRTPRPGQVPPVPSPODLLVEH 209

Search completed: May 27, 2003, 18:28:59
Job time: 17 secs